

Gencore version 5-1.4-p5_4578
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MM protein - protein search, using sw model

run on: April 15, 2003, 08:48:49 ; Search time 39 Seconds
(without alignments)
1175.339 Million cell updates/sec

title: US-09-831-061-2

perfect score: 344

sequence: 1 MKAIFVLNAAPKDNTWYAGG, DRRVIEVKGYKEYVTPQAG 344

scoring table: Oligo Gapop 60.0 , Gapext 60.0

searched: 908470 seqs, 133250620 residues

word size : 5

total number of hits satisfying chosen parameters: 25724

minimum DB seq length: 0

maximum DB seq length: 200000000

post-processing: Listing first 1000 summaries

Database :	Score	Query No.	Match Length	DB ID	Description
A_geneseq_101002,*	1:				
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/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1981 DAT:*	3:				
/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1982 DAT:*	4:				
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/SIDS2/gcgdata/geneseq/geneseq-emb1/AA2000 DAT:*	22:				
/SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001 DAT:*	23:				

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

8

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

Result No.	Score	Query			DB ID	Description
		Match	Length	DB		
1	344	100.0	344	21	AAE18994	A P40 polypeptide
2	344	100.0	344	21	AAE18804	A Klebsiella pneumoniae protein
3	344	100.0	344	21	AAE08825	A P40 polypeptide
4	344	100.0	344	21	AAE08317	An outer membrane protein
5	344	100.0	344	21	AAE08341	An outer membrane protein
6	344	100.0	344	21	AAY93341	Amino acid sequence
7	344	100.0	344	22	AAHG63698	Amino acid sequence
8	344	100.0	344	22	AAE67770	Amino acid sequence
9	344	100.0	344	23	ARM48395	Klebsiella pneumoniae protein
10	344	100.0	344	23	ARM47796	Klebsiella pneumoniae protein

84	2.6	1061	21	AAV80568	537	2.3	AAV03839
85	9	2639	22	ABG15016	550	14	AAR42085
86	8	2.3	10	ABP78543	2.3	550	AAR42254
87	8	2.3	15	AAR12480	159	8	Human p65 protein
88	8	2.3	26	AAV03840	160	8	Human p65 protein
89	8	2.3	41	AAV49097	161	8	Human NF-kappa-B p
90	8	2.3	43	AAV49096	162	8	Drosophila melanogaster
91	8	2.3	51	AAU62252	163	8	Human h-NUMB-R, H
92	8	2.3	52	ADP08909	164	8	Rat pan-s/tk recep-
93	8	2.3	60	ABB38355	165	8	Genswitch regulat-
94	8	2.3	60	ABB23542	166	8	Truncated GAL4 DBD
95	8	2.3	60	AAM58965	167	8	Human madt. protein
96	8	2.3	60	AAM71493	168	8	Candida albicans P
97	8	2.3	60	AAM19146	169	8	Genswitch regulat-
98	8	2.3	60	AAM31794	170	8	Human Cytoskeleton
99	8	2.3	60	ABG141306	171	8	Novel human diagno-
100	8	2.3	77	AAV41590	172	8	drophila melanogaster
101	8	2.3	86	AAG08968	173	8	GFP-NF-kappa-B fus-
102	8	2.3	86	AAM80159	174	8	PKB green fluorescein
103	8	2.3	86	ABB15278	175	8	NFKappaB p65 subun-
104	8	2.3	90	ABB71172	176	8	EGFP-NFkappaB fusi-
105	8	2.3	100	AAR4210	177	8	hNFKappaB EGFP fus-
106	8	2.3	103	ABB78542	178	8	Human protein SEQ
107	8	2.3	120	AAG22312	179	8	Novel human diagno-
108	8	2.3	128	AAM80159	180	8	drophila melanogaster
109	8	2.3	129	AAM19146	181	8	Human WART2, ortho-
110	8	2.3	131	AAG08967	182	8	Amid acid sequence
111	8	2.3	131	ABG46336	183	8	Balanus amphitrite
112	8	2.3	148	20	184	8	Amid acid sequence
113	8	2.3	167	AAY41598	185	8	Plasmodium falcipara
114	8	2.3	170	ABB61185	186	8	Protein encoded by
115	8	2.3	180	AAM19146	187	8	Hook region #2 con-
116	8	2.3	183	AAM19146	188	8	TTRP fragment. Sy-
117	8	2.3	187	AAW14579	189	8	Hook region #10 co-
118	8	2.3	188	AAW14580	190	8	trp Promoter lead-
119	8	2.3	190	AAW14569	191	8	Sequence encoded by
120	8	2.3	191	AAW14569	192	8	Peptide sequence o-
121	8	2.3	194	AAW14584	193	7	Hook region #9 con-
122	8	2.3	197	AAW40288	194	7	B. catarrhalis CD e-
123	8	2.3	202	ABB61097	195	7	Propionibacterium
124	8	2.3	204	18	196	7	A leader peptide N
125	8	2.3	206	18	197	7	Modified LE lead-
126	8	2.3	206	18	198	7	Propionibacterium
127	8	2.3	231	AAV8518	199	7	Human epidermal gr-
128	8	2.3	251	AAG23248	200	7	Peptide encoded by
129	8	2.3	254	AAG43170	201	7	MSI-1922.
130	8	2.3	254	AAG23247	202	7	Human zinc carboxy-
131	8	2.3	254	AAU72491	203	7	Arabidopsis thalia
132	8	2.3	280	AAG43168	204	7	N-terminal CT6 gly-
133	8	2.3	281	AAG23248	205	7	Peptide encoded by
134	8	2.3	283	AAV83088	207	7	Human zinc carboxy-
135	8	2.3	283	AAU29681	208	7	Arabidopsis thalia
136	8	2.3	283	AAU72491	209	7	Human zinc carboxy-
137	8	2.3	284	ABB4830	210	7	Arabidopsis thalia
138	8	2.3	313	AAU38739	211	7	Human zinc carboxy-
139	8	2.3	317	AAM40191	212	7	Arabidopsis thalia
140	8	2.3	317	AAG23249	213	7	Human zinc carboxy-
141	8	2.3	332	AAU17475	214	7	Arabidopsis thalia
142	8	2.3	353	ABB47447	215	7	Human zinc carboxy-
143	8	2.3	354	ABB69532	216	7	Arabidopsis thalia
144	8	2.3	355	AAR64226	217	7	Human zinc carboxy-
145	8	2.3	355	AAG65990	218	7	Arabidopsis thalia
146	8	2.3	358	AAG23249	219	7	Human zinc carboxy-
147	8	2.3	375	AAU7915	220	7	Arabidopsis thalia
148	8	2.3	392	ABB71946	221	7	Human zinc carboxy-
149	8	2.3	404	AAW68408	222	7	Arabidopsis thalia
150	8	2.3	437	AAU02965	223	7	Human zinc carboxy-
151	8	2.3	497	AAV94523	224	7	Arabidopsis thalia
152	8	2.3	498	AAV44562	225	7	Transforming growth
153	8	2.3	511	ABB19496	226	7	Drosophila melanogaster
154	8	2.3	516	AAV55928	227	7	Human secreted pro-
155	8	2.3	520	AAV01496	228	7	HCV II chimeric ep
156	8	2.3	520	AAV01497	229	7	ep

2.0	88	ABP03258	Human ORFX protein	303	2.0	169	AAW89682
2.0	89	ABP11383	Amino acid sequenc	304	7	172	14 AAR44753
2.0	90	AAPI0024	Human ORFX protein	305	7	172	15 AAR51659
2.0	95	AAW61279	Short fusion prote	306	7	172	17 AAR85169
2.0	95	AAB07939	Exodus protein.	307	7	172	19 AAW43409
2.0	96	AAR95690	A human C-C chemok	308	7	172	20 AAY43120
2.0	96	AAV93086	Liver expressed	309	7	172	20 AAW89886
2.0	96	AAV22669	Human Chemokine b	310	7	172	AAYW964
2.0	96	AAW57475	Human chemokine be	311	7	177	21 AAG07298
2.0	96	AAW44398	Human liver and ac	312	7	177	21 AAG53396
2.0	96	AAE41163	Human chemokine MI	313	7	177	21 AAY80194
2.0	96	AAV97074	Human chemokine be	314	7	178	22 AAB48072
2.0	96	AAV95535	Human chemokine MI	315	7	180	21 AAB24558
2.0	96	AAV31794	Human chemokine be	316	7	180	Plant SDF encoded
2.0	96	ABG60667	Amino acid sequenc	317	7	180	Arabidopsis thalia
2.0	96	AAO19996	Small inducible cy	318	7	182	Growth Factor LHL
2.0	96	AAE15750	Protein of human C	319	7	182	Arabidopsis thalia
2.0	96	AAG67371	Human chemokine be	320	7	182	Arabidopsis thalia
2.0	98	AAM19703	Amino acid sequenc	321	7	183	Streptococcus pneu
2.0	101	AAR95544	HCV I chimeric epi	322	7	184	Arabidopsis thalia
2.0	101	ABB39430	Peptide #6936 enco	323	7	185	Streptococcus pneu
2.0	101	ABB24202	Peptide #6201 enco	324	7	187	Human breast cance
2.0	101	AAM60110	Human brain expres	325	7	187	Arabidopsis thalia
2.0	101	ARM72742	Human bone marrow	326	7	187	Streptococcus pneu
2.0	101	AAM19703	Peptide #6137 enco	327	7	188	Arabidopsis thalia
2.0	101	ABB39430	Peptide #6990 enco	328	7	188	Streptococcus pneu
2.0	111	AAB31794	Human epidermal gr	329	7	189	Zea mays protein f
2.0	111	ABG42114	Zea mays protein f	330	7	190	Drosophila melanog
2.0	111	AAG50177	Arabidopsis thalia	331	7	190	Sequence encoded b
2.0	111	AAU40453	Propionibacterium	332	7	190	Sequence encoded b
2.0	111	AAM32953	Peptide #6950 enco	333	7	190	Nasseria meningit
2.0	111	ABG42546	Peptide #6208 enco	334	7	190	Neisseria gonorrhio
2.0	112	AAR74774	Human brain expres	335	7	190	Sequence of antigen
2.0	112	AAU40453	Human brain express	336	7	190	Streptococcus pneu
2.0	112	AAG42114	Zea mays protein f	337	7	190	Drosophila melanog
2.0	112	AAM50177	Arabidopsis thalia	338	7	190	Sequence encoded b
2.0	112	AAU40453	Propionibacterium	339	7	190	Sequence of antigen
2.0	112	ABB24209	Peptide #6950 enco	340	7	190	Sequence of an FMD
2.0	112	AAM60131	Protein #6208 enco	341	7	190	Sequence of antigen
2.0	112	AAU16172	Human novel secret	342	7	190	Streptococcus pneu
2.0	112	AAU16172	Neisseria gonorrhio	343	7	190	Arabidopsis thalia
2.0	113	ABB32973	Peptide #2682 enco	344	7	190	Arabidopsis thalia
2.0	113	AAU16172	Peptide #7010 enco	345	7	190	Arabidopsis thalia
2.0	113	ABG42569	Human peptide enco	346	7	190	Arabidopsis thalia
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2.0	113	AAU16172	Human novel secret	348	7	190	Arabidopsis thalia
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2.0	113	AAU16172	Peptide #2709 enco	350	7	190	Arabidopsis thalia
2.0	113	AAU16172	Protein #2643 enco	351	7	190	Arabidopsis thalia
2.0	113	AAU16172	Human peptide enco	352	7	190	Arabidopsis thalia
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2.0	113	AAU16172	Peptide #2655 enco	354	7	190	Arabidopsis thalia
2.0	113	AAU16172	Peptide #2748 enco	355	7	190	Arabidopsis thalia
2.0	113	AAU16172	Peptide #2633 enco	356	7	190	Arabidopsis thalia
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2.0	113	AAU16172	Human testicular sp. all	358	7	190	Arabidopsis thalia
2.0	113	AAU16172	Human reproductive a	359	7	190	Fusion protein con
2.0	113	AAU16172	Propionibacterium	360	7	190	Novel human diagno
2.0	113	AAU16172	Arabidopsis thalia	361	7	190	Novel human secret
2.0	113	AAU16172	Zea mays protein f	362	7	190	Arabidopsis thalia
2.0	113	AAU16172	Haemophilus influenzae	363	7	190	Fb-Fb-truncated "
2.0	113	AAU16172	Zea mays protein f	364	7	190	Human protein kina
2.0	113	AAU16172	Novel human diagno	365	7	190	zea mays protein f
2.0	113	AAU16172	Human secreted pro	366	7	190	zea mays protein f
2.0	113	AAU16172	Parietaria sp. all	367	7	190	zea mays protein f
2.0	113	AAU16172	Human SLT-2 homol	368	7	190	Rat neuronal Immed
2.0	113	AAU16172	Human nervous syst	369	7	190	Arabidopsis thalia
2.0	113	AAU16172	Streptococcus pneu	370	7	190	Arabidopsis thalia
2.0	113	AAU16172	zea mays protein f	371	7	190	Arabidopsis thalia
2.0	113	AAU16172	Osteogenic fusion	372	7	190	Fb-Fb-truncated " (
2.0	113	AAU16172	OP1A fusion protei	373	7	190	Human calcium tran
2.0	113	AAU16172	Human Osteogenic f	374	7	190	Novel human DNA-b1
2.0	113	AAU16172	Osteogenic protein	375	7	190	Consensus osteogen
2.0	113	AAU16172	COP5 gene product.	376	7	190	COP5 gene product.

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377	21	AAV5986	450	Sequence encoded b
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379	2.0	297	2.2	OPD fusion protein
380	2.0	ABG27036	452	Human osteogenic f
381	2.0	307	2.1	Osteogenic fusion
382	2.0	AAG3954	453	Osteogenic fusion
383	2.0	310	2.1	Osteogenic fusion
384	2.0	AAB14326	454	Osteogenic fusion
385	2.0	317	1.4	Osteogenic fusion
386	2.0	AAR4759	455	Osteogenic fusion
387	2.0	317	1.5	Osteogenic fusion
388	2.0	AAR51655	456	Osteogenic fusion
389	2.0	317	1.7	Osteogenic fusion
390	2.0	AAR5766	457	Osteogenic fusion
391	2.0	317	1.9	Osteogenic fusion
392	2.0	AAW44306	458	Novel human diagno
393	2.0	324	2.1	Osteogenic fusion
394	2.0	AAV3117	459	Osteogenic fusion
395	2.0	325	1.7	Osteogenic fusion
396	2.0	AAW03565	460	CBMP2B fusion pro
397	2.0	325	2.0	Human osteogenic f
398	2.0	AAV1413	461	CBMP2B fusion prot
399	2.0	325	2.1	Osteogenic fusion
400	2.0	AAW9683	462	CBMP2B fusion prot
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403	2.0	322	2.2	Osteogenic fusion
404	2.0	AAV11945	464	Osteogenic fusion
405	2.0	322	2.2	Osteogenic fusion
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407	2.0	322	2.2	Osteogenic fusion
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422	2.0	AAV17584	480	Osteogenic fusion
423	2.0	AAV17584	481	Osteogenic fusion
424	2.0	AAU01895	482	CD protein of Bran
425	2.0	AAU01895	483	Drosophila melanog
426	2.0	AAU01895	484	Novel human DNA-bi
427	2.0	AAU01895	485	N-terminal choline
428	2.0	AAU01895	486	Novel human diagno
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383	2.0	AAB14326	453	Osteogenic fusion
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385	2.0	AAR4759	454	Osteogenic fusion
386	2.0	317	1.5	Osteogenic fusion
387	2.0	AAW9683	455	Osteogenic fusion
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394	2.0	325	2.1	Osteogenic fusion
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453	2.0	AAV1683	512	Osteogenic fusion
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455	2.0	AAV1683	514	Osteogenic fusion
456	2.0	AAV1683	515	Osteogenic fusion
457	2.0	AAV1683	516	Osteogenic fusion
458	2.0	AAV1683	517	Osteogenic fusion
459	2.0	AAV1683	518	Osteogenic fusion
460	2.0	AAV1683	519	Osteogenic fusion
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463	2.0	AAV1683	522	Osteogenic fusion
464	2.0	AAV1683	523	Osteogenic fusion
465	2.0	AAV1683	524	Osteogenic fusion
466	2.0	AAV1683	525	Osteogenic fusion
467	2.0	AAV1683	526	Osteogenic fusion
468	2.0	AAV1683	527	Osteogenic fusion
469	2.0	AAV1683	528	Osteogenic fusion
470	2.0	AAV1683	529	Osteogenic fusion
471	2.0	AAV1683	530	Osteogenic fusion
472	2.0	AAV1683	531	Osteogenic fusion
473	2.0	AAV1683	532	Osteogenic fusion
474	2.0	AAV1683	533	Osteogenic fusion
475	2.0	AAV1683	534	Osteogenic fusion
476	2.0	AAV1683	535	Osteogenic fusion
477	2.0	AAV1683	536	Osteogenic fusion
478	2.0	AAV1683	537	Osteogenic fusion
479	2.0	AAV1683	538	Osteogenic fusion
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482	2.0	AAV1683	541	Osteogenic fusion
483	2.0	AAV1683	542	Osteogenic fusion
484	2.0	AAV1683	543	Osteogenic fusion
485	2.0	AAV1683	544	Osteogenic fusion
486	2.0	AAV1683	545	Osteogenic fusion
487	2.0	AAV1683	546	Osteogenic fusion
488	2.0	AAV1683	547	Osteogenic fusion
489	2.0	AAV1683	548	Osteogenic fusion
490	2.0	AAV1683	549	Osteogenic fusion
491	2.0	AAV1683	550	Osteogenic fusion
492	2.0	AAV1683	551	Osteogenic fusion
493	2.0	AAV1683	552	Osteogenic fusion
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495	2.0	AAV1683	554	Osteogenic fusion
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497	2.0	AAV1683	556	Osteogenic fusion
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502	2.0	AAU01895	561	Sequence encoded b
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521	2.0	AAU01895	580	Sequence encoded b
522	2.0	AAU01895	581	Sequence encoded b
523	2.0	AAU01895	582	Sequence encoded b
524	2.0	AAU01895	583	Sequence encoded b
525	2.0	AAU01895	584	Sequence encoded b
526	2.0	AAU01895	585	Sequence encoded b
527	2.0	AAU01895	586	Sequence encoded b
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529	2.0	AAU01895	588	Sequence encoded b
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531	2.0	AAU01895	590	Sequence encoded b
532	2.0	AAU01895	591	Sequence encoded b
533	2.0	AAU01895	592	Sequence encoded b
534	2.0	AAU01895	5	

522	7	802	20	AAY39033	M. tuberculosis fu	595	7	2.0	2665	22
523	7	802	23	AAU74592	Antigenic fusion p	596	7	2.0	2665	22
524	7	811	22	ABB62661	Drosophila melanog	597	7	2.0	2665	22
525	7	852	20	AYA31246	Murine ralGDS prot	598	7	2.0	2665	22
526	7	852	20	AYV30948	Human E3 ubiquitin	599	7	2.0	2665	23
527	7	852	21	AB23176	Human RalGDS (hRal	600	7	2.0	3192	22
528	7	854	20	AYA30949	Murine E3 ubiquiti	601	7	2.0	3266	22
529	7	883	22	AAM80136	Human protein SEQ	602	7	2.0	3536	22
530	7	903	20	AYA37116	Protein involved ¹	603	6	1.7	8	10
531	7	919	22	AAM79152	Human protein SEQ	604	6	1.7	8	10
532	7	931	22	AAM39815	Human polypeptide	605	6	1.7	8	22
533	7	937	23	ABP30468	Streptococcus poly	606	6	1.7	8	22
534	7	948	23	ABP27191	Streptococcus poly	607	6	1.7	8	22
535	7	972	23	AAU79039	Human macrophage c	608	6	1.7	8	22
536	7	972	23	AAU11934	Colony stimulating	609	6	1.7	9	17
537	7	972	23	AAU11935	Colony stimulating	610	6	1.7	9	21
538	7	972	23	AAU11936	Colony stimulating	611	6	1.7	9	22
539	7	972	23	AAU11937	Colony stimulating	612	6	1.7	9	22
540	7	972	23	AAU11938	Colony stimulating	613	6	1.7	10	17
541	7	972	23	AAU11939	Colony stimulating	614	6	1.7	10	17
542	7	972	23	AAU11940	Colony stimulating	615	6	1.7	10	22
543	7	972	23	AAU11941	Colony stimulating	616	6	1.7	10	22
544	7	972	23	AAU75385	Colony stimulating	617	6	1.7	10	22
545	7	975	22	AEE07144	Murine Kit/stem ce	618	6	1.7	10	22
546	7	975	22	AEE07148	Mutant murine Kit	619	6	1.7	10	22
547	7	975	22	AEE07149	Kit/stem cell	620	6	1.7	10	23
548	7	976	22	AEE07149	Murine human Kit/s	621	6	1.7	11	14
549	7	976	22	AEE00375	Human stem cell/gr	622	6	1.7	11	17
550	7	977	21	RAY51322	Bovine o-Kit bk-1	623	6	1.7	11	23
551	7	1016	22	AAU38901	C. trachomatis Ct8	624	6	1.7	11	23
552	7	1016	22	AAU76192	Actinoplanes sp. a	625	6	1.7	11	23
553	7	1021	19	AAU76192	Actinoplanes sp. ac	626	6	1.7	12	10
554	7	1023	23	AAM49562	Human homologue of	627	6	1.7	12	16
555	7	1039	22	ABB69116	Drosophila melanog	628	6	1.7	12	22
556	7	1055	22	ABG15479	Novel ovarian anti	629	6	1.7	12	22
557	7	1058	23	ABP1533	Human aortic carbo	630	6	1.7	13	15
558	7	1130	20	AAV13446	Human adipocyte en	631	6	1.7	13	21
559	7	1158	23	AAE22739	Novel human diaigno	632	6	1.7	13	23
560	7	1243	22	ABG21221	CP1A1-OVA-DD fusion	633	6	1.7	14	19
561	7	1265	23	AAU83954	Protein tyrosine-k	634	6	1.7	14	22
562	7	1298	16	AAR81937	FIT4 receptor tyro	635	6	1.7	15	17
563	7	1298	17	AAR90528	Amino acid sequenc	636	6	1.7	15	17
564	7	1298	21	AAV10365	Human Flt4 receptor	637	6	1.7	15	22
565	7	1298	21	AAV10746	Human tyrosine kin	638	6	1.7	15	22
566	7	1298	21	AAV10746	Mouse Flt-4 prote	639	6	1.7	15	23
567	7	1298	22	AAV97785	Human Flt-4 receptor	640	6	1.7	17	23
568	7	1298	22	AAB71111	Human Flt4/EGFR-3	641	6	1.7	17	23
569	7	1363	21	AAB9047	Human Flt4 receptor	642	6	1.7	18	23
570	7	1363	21	AAV90366	Human nestin prote	643	6	1.7	18	23
571	7	1363	21	AAV10747	Human Flt4 receptor	644	6	1.7	20	21
572	7	1363	22	AAV107604	Human Flt4L/VEGFR-	645	6	1.7	20	21
573	7	1406	21	AAB42916	Human ORFX ORF2680	646	6	1.7	20	21
574	7	1444	22	ABG15667	Novel human diaigno	647	6	1.7	20	21
575	7	1446	22	ABT1111	Drosophila melanog	648	6	1.7	20	21
576	7	1461	23	AAC14351	Human nestin protein	649	6	1.7	20	21
577	7	1487	23	AAO14352	Equine herpesvirus	650	6	1.7	20	21
578	7	1487	23	AAO14353	Equine herpesvirus	651	6	1.7	21	19
579	7	1487	23	AAO14354	Equine herpesvirus	652	6	1.7	21	19
580	7	1487	23	ABG15478	Novel human diaigno	653	6	1.7	20	21
581	7	1487	23	ABG15478	Novel human diaigno	654	6	1.7	20	21
582	7	1618	13	AAB20749	Novel human diaigno	655	6	1.7	20	21
583	7	1618	15	AAB60127	Human ORFX ORF1999	656	6	1.7	20	21
584	7	1618	22	AAU03898	Full length calcin	663	6	1.7	20	21
585	7	1693	22	ABB58927	Drosophila melanog	664	6	1.7	20	21
586	7	1909	22	ABG19127	Novel human diaigno	665	6	1.7	20	22
587	7	2129	22	AAB30525	Peptide fragment O	666	6	1.7	20	22
588	7	2129	22	AAB30525	Peptide fragment O	667	6	1.7	20	22
589	7	2220	21	AAB27205	Insert A to prevent	668	6	1.7	20	22
590	7	2220	21	AAB42235	Human cytomegalovi	669	6	1.7	20	22
591	7	2665	22	ABB28314	Delta6-16.0 (delta6	670	6	1.7	20	22
592	7	2665	22	ABB33490	Delta6-16.0 (delta6	671	6	1.7	20	22
593	7	2665	22	ABB33490	Human cytomegalovi	672	6	1.7	20	22
594	7	2665	22	AAM54270	Human brain expres	673	6	1.7	20	22

668	14	AAR33089	Human cytomegalovi	741	1.7	74	6	1.7	73	22	AAM86639
669	21	AAB4695	Human secreted pro	742	6	1.7	74	19	AAW0436		
670	34	AAR27562	Insert B-10 preven	743	6	1.7	74	21	AAV1020		
671	34	AAW48443	HHV8 ORF K8.1 biva	744	6	1.7	74	22	AAU61732		
672	21	AAV5504	Human cytomegalovi	745	6	1.7	76	21	AAB4024		
673	14	AAR33083	Arabidopsis thalica	746	6	1.7	76	22	AAB52682		
674	35	AAC22929	Arabidopsis thalica	747	6	1.7	76	22	AAG91916		
675	21	AAG57714	Arabidopsis thalica	748	6	1.7	78	21	AAB24990		
676	40	AAG20091	Arabidopsis thalica	749	6	1.7	78	21	AAC25095		
677	41	AAK33090	Human cytomegalovi	750	6	1.7	78	22	ABZ26149		
678	41	AAK33092	Human cytomegalovi	751	6	1.7	81	23	ABP0215		
679	22	AAE03992	Human gene 42 enco	752	6	1.7	81	23	ABP04105		
680	19	AAW42515	Peptide derived fr	753	6	1.7	83	22	ABP68955		
681	22	ABB29611	Peptide #2262 enco	754	6	1.7	83	22	AAM44488		
682	22	ABB34194	Peptide #2299 enco	755	6	1.7	85	21	AAC37573		
683	42	ABB20008	Protein #2207 enco	756	6	1.7	85	22	AAU59296		
684	22	AAW5591	Human brain express	757	6	1.7	87	21	AAU61758		
685	22	AAM67977	Human bone marrow	758	6	1.7	88	23	ABP33238		
686	22	AAM15795	Peptide #2229 enco	759	6	1.7	86	21	AAG12105		
687	22	AAM28104	Peptide #2341 enco	760	6	1.7	86	22	AAU59180		
688	22	AAM03330	Peptide #2212 enco	761	6	1.7	87	21	AAY93410		
689	42	ABG37514	Human peptide enco	762	6	1.7	87	22	ABB69259		
690	43	AAV10120	YhdD repeat sequen	763	6	1.7	87	22	AAU60312		
691	49	AAW5269	Human immune/haema	764	6	1.7	88	23	ABP34161		
692	50	AAM32996	Human ORF1369 prot	765	6	1.7	88	23	AAB2191		
693	23	ABP32754	Human ORF1727 prot	766	6	1.7	89	19	AAM9857		
694	14	AAR31091	Human cytomegalovi	767	6	1.7	89	22	AAB69512		
695	52	AAG0444	Arabidopsis thalica	768	6	1.7	90	16	AAR80175		
696	52	AAG51693	Arabidopsis thalica	769	6	1.7	90	22	AAC10715		
697	53	AAO0413	Human polypeptide	770	6	1.7	90	22	AAE10116		
698	52	AAC19720	Arabidopsis thalica	771	6	1.7	90	22	AAE21472		
699	21	AAG61016	Arabidopsis thalica	772	6	1.7	92	21	AAM68386		
700	57	AAU0796	Propionibacterium	773	6	1.7	93	21	AAB59908		
701	51	AAR33091	Propionibacterium	774	6	1.7	93	21	AAB59908		
702	52	AAG51693	Propionibacterium	775	6	1.7	93	21	AAB59908		
703	58	ABB4042	Peptide #7348 enco	776	6	1.7	93	22	AAB30898		
704	58	ABB24544	Protein #6543 enco	777	6	1.7	93	22	ABB3080		
705	58	AAU0792	Human brain express	778	6	1.7	93	23	ABG8859		
706	58	AAM73467	Human bone marrow	779	6	1.7	93	22	AAM56862		
707	57	AAU0796	Propionibacterium	780	6	1.7	93	22	AAM62449		
708	58	AAU0796	Peptide #702 enco	781	6	1.7	93	22	AAM11078		
709	59	ABP11067	Human peptide enco	782	6	1.7	93	22	AAM2572		
710	62	AAB45407	Human ORFX protein	783	6	1.7	93	22	AAM04779		
711	62	AAU66864	Human secreted Pro	784	6	1.7	94	21	AAG9219		
712	62	AAU45452	Propionibacterium	785	6	1.7	95	21	AAG61977		
713	63	AAU45452	Arabidopsis thalica	786	6	1.7	95	22	AAU7703		
714	63	AAG20090	Human secreted pro	787	6	1.7	95	22	AAM66608		
715	63	AAU03612	Hepatitis B virus	788	6	1.7	97	21	AAG17572		
716	63	AAU81132	Hepatitis B virus	789	6	1.7	97	22	AAU03179		
717	63	AAU17026	Human ORFX protein	790	6	1.7	98	22	ABD69550		
718	64	AAU81134	Propionibacterium	791	6	1.7	101	22	AAG09938		
719	65	AAU48572	Arabidopsis thalica	792	6	1.7	101	22	AAG9764		
720	63	ABP1024	C-terminaly trunc	793	6	1.7	102	22	AAB19117		
721	63	AAU17026	Arabidopsis thalica	794	6	1.7	102	22	AAR80084		
722	68	AAU26192	Human immune/haema	795	6	1.7	102	22	AAR94315		
723	68	AAU81134	Hepatitis B virus	796	6	1.7	103	22	ABD67477		
724	68	ABP10344	Propionibacterium	797	6	1.7	104	21	AAG19719		
725	65	AAU1024	P. funiculosum acti	798	6	1.7	104	21	ABG51014		
726	63	AAU17026	Arabidopsis thalica	799	6	1.7	104	22	ABG250614		
727	67	AAE17026	Novel human respir	800	6	1.7	105	16	AAR94314		
728	68	AAU00779	Cytomegalovirus (C.	801	6	1.7	105	16	ABB55314		
729	70	ABG02382	Arabidopsis thalica	802	6	1.7	105	20	AAY36869		
730	68	AAU72000	Novel human diagno	803	6	1.7	105	21	AAG19719		
731	71	AAU12538	Human ORFX protein	804	6	1.7	105	22	AAM25500		
732	69	AAU17026	Arabidopsis thalica	805	6	1.7	105	22	AAB94156		
733	69	AAU17026	Human secreted pro	806	6	1.7	105	23	ABP05668		
734	70	AAU00779	Drosophila melanog	807	6	1.7	105	22	AAB67747		
735	72	ABG61454	Propionibacterium	808	6	1.7	105	22	AAU314160		
736	72	ABG26938	Novel human diagno	809	6	1.7	105	22	M. vaccae antigen		
737	73	AAU26900	Arabidopsis thalica	810	6	1.7	111	22	AAU14900		
738	73	AAU03301	Human secreted pro	811	6	1.7	113	19	AAW60153		
739	73	ABB68706	Drosophila melanog	812	6	1.7	113	20	M. vaccae antigen		
740	1.7	ABG25702	Novel human diagno	813	6	1.7	113	20	AAU14900		

814	1.7	113	20	AAY36969	887	6	1.7	AAU02102	
815	6	1.7	113	23	AAU76277	888	6	1.7	ABP10963
816	6	1.7	113	23	ABB75506	889	6	1.7	ARR22999
817	6	1.7	114	7	AAP60386	890	6	1.7	AAG13637
818	6	1.7	114	21	AAP94770	891	6	1.7	ABE68985
819	6	1.7	114	21	AAB20585	892	6	1.7	AAQ05029
820	6	1.7	116	16	AAR80117	893	6	1.7	AAW09017
821	6	1.7	116	16	AAR80189	894	6	1.7	ABP04254
822	6	1.7	116	21	AAB37425	895	6	1.7	ABG04498
823	6	1.7	116	21	AAB37426	896	6	1.7	ABG11775
824	6	1.7	117	22	AAG81206	897	6	1.7	ABG25379
825	6	1.7	117	22	AAU52251	898	6	1.7	ABG27169
826	6	1.7	118	21	AAB3493	899	6	1.7	AAR23000
827	6	1.7	118	22	AAU01269	900	6	1.7	Human adhesin 3
828	6	1.7	118	22	AAO01269	901	6	1.7	Human camellia
829	6	1.7	119	21	AAV37427	902	6	1.7	Novel human diagno
830	6	1.7	119	21	AAU74499	903	6	1.7	Novel human diagno
831	6	1.7	120	22	AAU043965	904	6	1.7	Novel human diagno
832	6	1.7	120	22	AAU09170	905	6	1.7	Novel human diagno
833	6	1.7	121	22	ABG27743	906	6	1.7	D. Inimitis aromati
834	6	1.7	121	22	ABB52527	907	6	1.7	Human prostate tum
835	6	1.7	121	22	AAU02146	908	6	1.7	Arabidopsis thalia
836	6	1.7	121	23	AAU74499	909	6	1.7	Pathogen response
837	6	1.7	122	21	AAG11997	910	6	1.7	Arabidopsis thalia
838	6	1.7	122	22	ABB88984	911	6	1.7	Arabidopsis thalia
839	6	1.7	122	22	AAU22040	912	6	1.7	Arabidopsis thalia
840	6	1.7	122	22	AAU81517	913	6	1.7	Arabidopsis thalia
841	6	1.7	122	22	AAU51103	914	6	1.7	Arabidopsis thalia
842	6	1.7	122	22	AAU59168	915	6	1.7	Arabidopsis thalia
843	6	1.7	122	23	AAC17362	916	6	1.7	Arabidopsis thalia
844	6	1.7	124	18	AAW14582	917	6	1.7	Arabidopsis thalia
845	6	1.7	124	21	AAG12104	918	6	1.7	Rice fungal resist
846	6	1.7	125	7	AAP0285	919	6	1.7	Protein encoded by
847	6	1.7	125	10	AAW94765	920	6	1.7	Propionibacterium
848	6	1.7	125	10	AAW90283	921	6	1.7	Novel human diagno
849	6	1.7	125	10	AACT35777	922	6	1.7	Pathogen response
850	6	1.7	125	22	AAQ01736	923	6	1.7	Arabidopsis thalia
851	6	1.7	126	21	AAW09850	924	6	1.7	Arabidopsis thalia
852	6	1.7	128	21	AAW1672	925	6	1.7	Blackcurrant RIBL
853	6	1.7	129	21	AAU139842	926	6	1.7	Arabidopsis thalia
854	6	1.7	129	21	AAU94765	927	6	1.7	Arabidopsis thalia
855	6	1.7	130	21	AAY85182	928	6	1.7	Arabidopsis thalia
856	6	1.7	130	23	ABB80370	929	6	1.7	Arabidopsis thalia
857	6	1.7	131	18	AAW14583	930	6	1.7	Novel human diagno
858	6	1.7	131	21	AAB51671	931	6	1.7	Zea mays protein f
859	6	1.7	131	21	AAU75070	932	6	1.7	Propionibacterium
860	6	1.7	131	21	AAU5352	933	6	1.7	Human prostate can
861	6	1.7	131	21	AAU60290	934	6	1.7	Arabidopsis thalia
862	6	1.7	131	21	AAU44995	935	6	1.7	Arabidopsis thalia
863	6	1.7	132	19	AAW1672	936	6	1.7	Arabidopsis thalia
864	6	1.7	132	21	AAU75352	937	6	1.7	Arabidopsis thalia
865	6	1.7	132	23	ABG60260	938	6	1.7	Arabidopsis thalia
866	6	1.7	133	22	AAU43804	939	6	1.7	Staphylococcus proteas
867	6	1.7	133	22	AAU44998	940	6	1.7	D. immitis aromati
868	6	1.7	133	22	AAU94541	941	6	1.7	Human ORF X protein
869	6	1.7	133	22	AAM25751	942	6	1.7	Blackcurrant fruit
870	6	1.7	133	22	AAM13639	943	6	1.7	Human kinase like
871	6	1.7	133	22	AAG33199	944	6	1.7	Prochymosin N-term
872	6	1.7	133	22	AAU19874	945	6	1.7	Mouse odorant blind
873	6	1.7	133	23	ABG61731	946	6	1.7	Arabidopsis thalia
874	6	1.7	133	23	AAE01761	947	6	1.7	AAW17055
875	6	1.7	136	21	AAG09337	948	6	1.7	AAU16622
876	6	1.7	136	21	AAG09336	949	6	1.7	AAU2214
877	6	1.7	136	21	AAG39162	950	6	1.7	AAO13099
878	6	1.7	137	22	AAU81184	951	6	1.7	Human ORF X ORF1867
879	6	1.7	138	21	AAG09849	952	6	1.7	AAU33944
880	6	1.7	138	23	ABB49190	953	6	1.7	ABP04807
881	6	1.7	139	21	AAG09336	954	6	1.7	AAW17055
882	6	1.7	139	21	AAC39162	955	6	1.7	AAU13198
883	6	1.7	139	22	AAG81184	956	6	1.7	ABP040419
884	6	1.7	140	18	AAW22493	957	6	1.7	ABP58786
885	6	1.7	140	22	AAU65261	958	6	1.7	AAU336793
886	6	1.7	140	22	AAM93094	959	6	1.7	AAU37229
							1.7	173	AAU37542

960	12	AAR12394	Pre-S antigen. He	XX
961	12	AAR15658	HBSAg pre-S region	DR
962	12	AAR15617	HBSAg pre-S region	DR
963	12	AAR15221	HBSAg pre-S region	XX
964	12	AAR15222	HBSAg pre-S region	PT
965	12	AAR23165	Pre-S gene region	PT
966	12	AAR23166	Pre-S gene region	PT
967	12	AAR23167	Pre-S gene region	PT
968	22	AAU39003	Propionibacterium	XX
969	23	ABG47283	Human peptide enco	PS
970	12	AAR10664	Portion Of rat PAC	XX
971	15	AAR51875	Human p3 amino ac	CC
972	17	ABB70022	Drosophila melanog	CC
973	17	ABG12341	Novel human diagno	CC
974	17	ABP37997	Staphylococcus epi	CC
975	17	183	Arabidopsis thalia	CC
976	21	AAG66663	Arabidopsis thalia	CC
977	17	184	AAG04224	CC
978	21	AAG21302	Arabidopsis thalia	CC
979	21	AAG21697	Arabidopsis thalia	CC
980	22	ABG18844	Novel human diagno	CC
981	22	AAU12651	Novel human secret	CC
982	23	ABB06074	Human NS protein s	CC
983	21	AAG28642	Arabidopsis thalia	CC
984	22	AAU20419	Human secreted pro	CC
985	17	AAY74763	Neisseria gonorrhoe	XX
986	17	AAY74765	meningit	SQ
987	23	ABP38950	Staphylococcus epi	Sequence
988	17	191	Cryptosporidium Pa	344 AA;
989	17	192	Novel human diagno	100.0%
990	17	193	Arabidopsis thalia	Score 344;
991	17	193	Peptide #4550 enco	DB 21;
992	17	193	Peptide #4613 enco	Length 344;
993	22	ABB21133	Protein #4449 enco	Pred. No. 0;
994	17	192	Human brain expres	Mismatches 0;
995	17	193	Human bone marrow	Indels 0;
996	17	193	Peptide #4516 enco	Gaps 0;
997	22	ABB31899	Peptide #4511 enco	
998	17	193	Peptide #4517 enco	
999	23	ABG39918	Human Peptide enco	
1000	17	193	Human ovarian anti	
	194	22	AAV49916	

ALIGNMENTS

RESULT 1			
AAB18994			
	standard;	Protein:	344 AA.
	AAB18994;		
	AC		
	XX		
	08-FEB-2001 (first entry)		
	XX		
	A PAO nolwendt (as of 9/16/2011)		

卷之三

immune response; mononuclear blood cell; tumour necrosis factor-alpha; interleukin-12; antitumour; cancer.

RESULT 3

AAB118804 standard; Protein; 344 AA.
XX

AC : AAB-6504 ;
 XX
 XX
 DT DT
 XX XX
 DE DE
 XX XX
 A Klebsiella pneumoniae P40 polypeptide.
 P40 polypeptide; membrane fraction; antigen; hapten; immune response;
 infectious disease; cancer; Paranyxoviruse infection;
 respiratory syncytial virus; parainfluenza.
 Klebsiella pneumoniae.
 XX OS OS
 XX PN PN
 WO200054789-A1.
 XX

PD	21-SEP-2000.			
XX	15-MAR-2000; 2000W0-FR00622.			
PF				
PR	15-MAR-1999;			
XX	PA (FABR) FABRE MEDICAMENT SA PIERRE.			
PA				
XX	Libon C, Corvai N, N'Guyen TN, Beck A, Bonnefoy J;			
PI				
XX	WPI: 2000-587476/55.			
DR	N-PDBB; AAA75881.			
DR				
XX	Use of Klebsiella membrane fraction as adjuvant, for e.g. antitumor or antiviral vaccines, to direct a Th1, or mixed, immune response against associated antigen			
XX	Disclosure: Page 28-29; 36pp; French.			
CC	The present sequence represents a Klebsiella pneumoniae P40 polypeptide.			
CC	The protein is isolated from a membrane fraction. The specification describes the use of a membrane fraction from Klebsiella pneumoniae, associated with an antigen or hapten, for preparation of a pharmaceutical composition that directs a Th1, or mixed Th1/Th2 immune response. The composition is used for treatment or prevention of infectious diseases (viral, bacterial, fungal or parasitic) or cancers, most especially infections by paramyxoviruses, specifically respiratory syncytial virus or parainfluenza.			
XX	Sequence 344 AA;			
Qy	1 MKAIFYVLAAPKDNNTWYAGGKLGMWSOYHDTGFYGNFGQNNGPTRDQLGAGAEGGYQVN 60			
Db	1 MKAIFYVLAAPKDNNTWYAGGKLGMWSOYHDTGFYGNFGQNNGPTRDQLGAGAEGGYQVN 60			
Qy	61 PYLGFFEMGYDWLGRMAYKGSYDNGAKFAQGVYQTLAKGYPTTDDLDIYTRIGGMNWRADS 120			
Db	61 PYLGFFEMGYDWLGRMAYKGSYDNGAKFAQGVYQTLAKGYPTTDDLDIYTRIGGMNWRADS 120			
Qy	121 KGNYASTGVERSEHTGTGSPVFAAGGSEWAETRDITRLTLEYQWNНИGDAFTVGTTRPDNGM 180			
Db	121 KGNYASTGVERSEHTGTGSPVFAAGGSEWAETRDITRLTLEYQWNНИGDAFTVGTTRPDNGM 180			
Qy	181 LSLGSYRFQEDAAPPVVARAPAPAPEVATKHFTLKSDVLNFENFATLKPEQQALDQLY 240			
Db	181 LSLGSYRFQEDAAPPVVARAPAPAPEVATKHFTLKSDVLNFENFATLKPEQQALDQLY 240			
Qy	241 TQLSNMDPKDGSAYVLLGYDTRIGSEAYNQLSERKQAQSVDYLVAKGIPAKGKISARGMGE 300			
Db	241 TQLSNMDPKDGSAYVLLGYDTRIGSEAYNQLSERKQAQSVDYLVAKGIPAKGKISARGMGE 300			
Qy	301 SNPVTGNTCDNVKARAALIDCLAFDRVEIEVKYKEVTTQPG 344			
Db	301 SNPVTGNTCDNVKARAALIDCLAFDRVEIEVKYKEVTTQPG 344			
RESULT 3	AAB08825			
ID	AAB08825 standard; Protein: 344 AA..			
AC				
XX	02-JAN-2001 (first entry)			
DE	A P40 polypeptide (an outer membrane protein A (OmpA)).			
XX	P40; outer membrane protein A; OmpA; immunogen; cytokine; growth factor; hormone; tumour-specific marker; vaccine; cancer; contraceptive.			
XX	AAE08825; standard; Protein: 344 AA..			
AC				
XX	02-JAN-2001 (first entry)			
RESULT 4				
ID	AAB08317 standard; Protein: 344 AA.			
AC				
XX	AAE08317;			
XX	04-DEC-2000 (first entry)			
DE	An outer membrane protein A (OmpA) designated DAB			

Outer membrane protein A; OmpA; P40; cytotoxic T cell response; CTL response; tumour cell; vaccine; infection; tumour; melanoma; genetic vaccine.	ID XX AC AAB08341; XX XX DT 04-DEC-2000 (first entry)
Klebsiella pneumoniae.	XX DE An outer membrane protein A (OmpA), designated P40. XX KW Outer membrane protein A; OmpA; P40; cytotoxic T cell response; tumour; CTL response; tumour cell; vaccine; melanoma; genetic vaccine.
WO20048628-A1.	XX KW XX OS Klebsiella pneumoniae.
24-AUG-2000.	XX PN WO20048629-A1.
17-FEB-2000; 99FR-0001917.	XX PD 24-AUG-2000
(FABR) FABRE MEDICAMENT SA PIERRE.	XX PF 17-FEB-2000; 2000WO-FR00394. XX PR 17-FEB-1999; 99FR-0001917.
Reno T., Bonneføy J;	XX PA (FABR) FABRE MEDICAMENT SA PIERRE. XX P1 RENO T., ROMERO P., MICONNET I., CAROTTINI J., BONNEFOY J.; XX WPI: 2000-549238/50. DR N-PSDB; AA63956. XX WPI: 2000-549238/50. DR N-PSDB; AA63956.
Use of enterobacterial outer membrane protein A in vaccines, useful for inducing cytotoxic T cell responses, useful for treating or preventing infections and tumors -	XX PT Use of enterobacterial outer membrane protein A in vaccines, used to treat or prevent melanoma, includes melanoma-specific peptide and induces cytotoxic lymphocyte response - XX PS Claim 6; Page 30-31; 35pp; French. XX CC The present sequence represents a Klebsiella pneumoniae outer membrane protein A (OmpA), designated P40. The enterobacterial OmpA polypeptide, or its fragments, is used for preparing a composition that induces, or increases, the cytotoxic T cell (CTL) response against an infectious agent or tumour cell. Compositions containing OmpA, optionally mixed with or coupled to a suitable antigen or hapten, are used as vaccines for treatment or prevention of infections caused by viruses, bacteria, fungi and parasites or tumors, particularly where associated with an antigen and specifically melanoma. Nucleic acids that encode OmpA (or its fusion with antigens or haptens) are useful as genetic vaccines again for treating infections and tumors. Sequence 344 AA; Query Match 100.0%; Score 344; DB 21; Length 344; Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0; Matches 344; Conservative 0; Gaps 0; Sequence 344 AA;
Claim 7; Page 38-39; 45pp; French.	Query Match 100.0%; Score 344; DB 21; Length 344; Best Local Similarity 100.0%; Pred. No. 0; Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
The present sequence represents a Klebsiella pneumoniae outer membrane protein A (OmpA), designated P40. The enterobacterial OmpA polypeptide, or its fragments, is used for preparing a composition that induces, or increases, the cytotoxic T cell (CTL) response against an infectious agent or tumour cell. Compositions containing OmpA, optionally mixed with or coupled to a suitable antigen or hapten, are used as vaccines for treatment or prevention of tumors, particularly where associated with an antigen and specifically melanoma. Nucleic acids that encode OmpA (or its fusion with antigens or haptens) are useful as genetic vaccines again for treating tumors.	Qy 1 MKAFVLNAAPKDNTWYAGKGLGRSQYHDTGFYNGFQNNGPRTNDLQAGAFCGGYQVN 60 1 MKAFVLNAAPKDNTWYAGKGLGRSQYHDTGFYNGFQNNGPRTNDLQAGAFCGGYQVN 60 61 PYLGFMGYDWLGRMAYKGSDVNGAKAQVQLTAKLGPITDDLDIVTRGGMWRADS 120 61 PYLGFMGYDWLGRMAYKGSDVNGAKAQVQLTAKLGPITDDLDIVTRGGMWRADS 120 121 KGNYASTGYSRSERDTGSPVFAFGVEAVTRDIATRLRELYQWNINIGDAQTGTRPDGM 180 121 KGNYASTGYSRSERDTGSPVFAFGVEAVTRDIATRLRELYQWNINIGDAQTGTRPDGM 180 181 LSLOGSYRFQDAAVPPAPAPAPEVATKHTLKSVDLFNFNKATLKPEGQQLDOLY 240 181 LSLOGSYRFQDAAVPPAPAPAPEVATKHTLKSVDLFNFNKATLKPEGQQLDOLY 240 241 TOLSNMDPDKGSAVVLGYTDRGSEAYNQLSSEKRAQSVDLVAKGIPAGKISARGMGE 300 241 TOLSNMDPDKGSAVVLGYTDRGSEAYNQLSSEKRAQSVDLVAKGIPAGKISARGMGE 300 301 SPPVTGNTCDNWKARAALIDCLAPDRVEIYGKKEVVTQDG 344 301 SPPVTGNTCDNWKARAALIDCLAPDRVEIYGKKEVVTQDG 344 Query Match 100.0%; Score 344; DB 21; Length 344; Best Local Similarity 100.0%; Pred. No. 0; Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
WO200048628-A1.	Qy 61 PYLGFMGYDWLGRMAYKGSDVNGAKAQVQLTAKLGPITDDLDIVTRGGMWRADS 120 Db 61 PYLGFMGYDWLGRMAYKGSDVNGAKAQVQLTAKLGPITDDLDIVTRGGMWRADS 120 Qy 121 KGNYASTGYSRSERDTGSPVFAFGVEAVTRDIATRLRELYQWNINIGDAQTGTRPDGM 180 Db 121 KGNYASTGYSRSERDTGSPVFAFGVEAVTRDIATRLRELYQWNINIGDAQTGTRPDGM 180 Qy 181 LSQGVSYRFQDAAVPPAPAPAPEVATKHTLKSVDLFNFNKATLKPEGQQLDOLY 240 Db 181 LSQGVSYRFQDAAVPPAPAPAPEVATKHTLKSVDLFNFNKATLKPEGQQLDOLY 240 Qy 241 TOLSNMDPDKGSAVVLGYTDRGSEAYNQLSSEKRAQSVDLVAKGIPAGKISARGMGE 300 Db 241 TOLSNMDPDKGSAVVLGYTDRGSEAYNQLSSEKRAQSVDLVAKGIPAGKISARGMGE 300 Qy 301 SNPVGTGNTCDNWKARAALIDCLAPDRVEIYGKKEVVTQDG 344 Qy 301 SNPVGTGNTCDNWKARAALIDCLAPDRVEIYGKKEVVTQDG 344 Qy 301 SNPVGTGNTCDNWKARAALIDCLAPDRVEIYGKKEVVTQDG 344 Qy 301 SNPVGTGNTCDNWKARAALIDCLAPDRVEIYGKKEVVTQDG 344

RESULT 5

Db	301	SNPTGNTCDNVKARAALIDCLAPDRRYEIVKGYKEVVTQPG	344	
RESULT 6				
AY93341				
ID AY93341 standard; Protein:	344 AA.			
XX				
AC AY93341;				
XX				
DT 04-SEP-2000 (first entry)				
DE Amino acid sequence of a Klebsiella P40 protein.				
XX				
KW P40 protein; outer membrane protein A; OmpA; antigen-presenting cell; dendritic cell; antigen delivery; immune response; allergy; graft rejection; tumour-associated antigen; autoimmune disease; central nervous system disease; inflammation; cardiovascular disease; infection; immune deficiency.				
XX				
OS Klebsiella pneumoniae.				
XX				
PN WO2000027432-A1.				
XX				
PD 18-MAY-2000.				
XX				
PF 08-NOV-1999; 99WO-FR02734.				
XX				
PR 06-NOV-1998; 98FR-0014007.				
XX				
PA (FABR) FABRE MEDICAMENT SA PIERRE.				
XX				
PI Bonnefey J, Lecomet S, Aubry J, Jeannin P, Baussant T;				
XX				
DR 2000-387342/33.				
DR N-PSDB; AIA15438.				
XX				
PT Use of enterobacterial outer membrane protein A for delivering active substances, particularly immunogens for treating or preventing e.g. cancer, to antigen presenting cells				
PT				
PT				
XX				
PS Claim 9; Page 28-29; 31PP; French.				
XX				
CC The present sequence represents a P40 protein. The protein is an outer membrane protein A (OmpA). The protein is used in pharmaceutical compositions for specific targeting of an active substance to antigen presenting cells (APCs), especially dendritic cells. OmpA binds specifically to APCs and is internalized by them (in contrast to other protein carriers such as tetanus toxoid). The OmpA protein is used to deliver an antigen or haptene to modify (specifically to improve) an immune response, especially for treatment or prevention of cancers (particularly those that express a associated antigen), autoimmune disease, allergy, graft rejection, cardiovascular or central nervous system diseases, inflammation, infection or immune deficiency.				
CC Sequence 344 AA;				
CC Query Match Best Local Similarity Score 344; DB 21; Length 344; Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
CC Qy 1 MKAIFVLAAPKDNTWAGGKLGNQHDFGYNGFQNNGPRTNDQLGAGAGGGQVN 60				
CC Db 1 MKAIFVLAAPKDNTWAGGKLGNQHDFGYNGFQNNGPRTNDQLGAGAGGGQVN 60				
CC Qy 61 PYLGFEMGYWLGRLWAKGYSVNDGAFKAQGVLTAKLGYPITDLDIYTRLGMMWRADS 120				
CC Db 61 PYLGFEMGYWLGRLWAKGYSVNDGAFKAQGVLTAKLGYPITDLDIYTRLGMMWRADS 120				
CC Qy 121 KGNASTGVSRSERHDTCGSPVAGGVAVTRDATRLEYQWNINIGDAGTVTRPDNGM 180				
CC Db 121 KGNASTGVSRSERHDTCGSPVAGGVAVTRDATRLEYQWNINIGDAGTVTRPDNGM 180				
CC Qy 1 MKAIFVLAAPKDNTWAGGKLGNQHDFGYNGFQNNGPRTNDQLGAGAGGGQVN 60				
CC Sequence 344 AA;				
Query Match Best Local Similarity Score 344; DB 22; Length 344; Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				

QY	301	SNPTGTNTCDNVKARAALIDCLA	DRVIEVGKVEVTPAG	344
Db	301	SNPTGTNTCDNVKARAALIDCLAP	DRVIEVGKVEVTPAG	344
AAB67770				
AAB67770				
11-JUN-2001	(first entry)			
Amino acid sequence of an outer membrane protein A (OmpA) P40.				
Outer membrane protein A; OmpA; P40; enterobacteria; nasal composition; respiratory syncytial virus; RSV; RSV infection; lung; respiratory tract; vaccine.				
Klebsiella pneumoniae.				
WO200121203-A1.				
29-MAR-2001.				
22-SEP-2000; 2000WO-FR02626.				
23-SEP-1998; 99FR-0011848.				
(FABR) FABRE MEDICAMENT SA PIERRE.				
Corviale N, Goestch L;				
WPI; 2001-257929/26.				
N-PSDB; AAF80152.				
Vaccine against respiratory syncytial virus, comprises enterobacterial outer membrane protein and viral immunogen, provides protective response throughout the respiratory tract.				
Claim 3; Page 28-29; 39pp; French.				
The present sequence represents an outer membrane protein A (OmpA), designatated P40. Enterobacterium OmpA proteins, associated with an immunogenic peptide from respiratory Syncytial virus (RSV), are used to prepare a nasal composition that induces a protective response, against RSV infection in the upper and lower (lung) respiratory tract. OmpA potentiates the immune response to some immunogenic peptides, eliminating the need for adjuvants. The method is useful for producing vaccines for prevention or treatment of RSV infections.				
RESULT 9				
AA48395	ID	AA48395 standard; protein;	344 AA.	
XX	XX			
AA48395;	AC			
XX	XX			
Klebsiella pneumoniae outer membrane protein, OmpA.	DE			
OmpA; outer membrane protein; cytostatic; cancer; tumour antigen.	KW			
XX	XX			
Klebsiella pneumoniae.	OS			
XX	PN			
WO20012959-A1.	XX			
08-NOV-2001.	PD			
XX	PF			
03-MAY-2001; 2001WO-FR01348.	XX			
PR	04-MAY-2000; 2000ER-0005702.			
XX	PA			
(FABR) FABRE MEDICAMENT SA PIERRE.	XX			
PI	Reno T, Invernizzi L, Bonnefond J;			
XX	DR			
WPI; 2002-06490/09.	XX			
Composition, useful for treatment and prevention of cancer, also for detecting tumor antigens, comprises an outer membrane protein and tumor lysate -	PT			
XX	PT			
PS	Claim 5; Page 25-26; 32pp; French.			
XX				
CC	The present invention relates to a pharmaceutical composition, comprising an Outer Membrane Protein (e.g., OmpA), associated with a lysate of CC autologous and/or heterologous tumour cells. The present sequence is one CC such OmpA from Klebsiella pneumoniae. The composition is useful for the CC treatment of cancers, particularly where associated with tumour antigens CC and for detecting tumour antigens.			
XX				

QY 1 MKAIFYLNAAPPKDNTWYAGGKLIGSQYHDTGYGNGFQNNGPTRNDQLGAGAFFGGYQVN 60
 Db 1 MAIFVNLNAPKDNTWYAGGKLIGSQYHDTGYGNGFQNNGPTRNDQLGAGAFFGGYQVN 60
 QY 61 PYLGFFENGDWLMGRMAYKGSYDNGAKFAQGVQLTAKLGPITDDLDIYTRLGGMWIRAL ..J
 Db 61 PYLGFFENGDWLMGRMAYKGSYDNGAKFAQGVQLTAKLGPITDDLDIYTRLGGMWIRADS 120
 QY 61 PYLGFFENGDWLMGRMAYKGSYDNGAKFAQGVQLTAKLGPITDDLDIYTRLGGMWIRADS 120
 QY 121 KGNVASTGVSRSEHDTGVSPIAGGYEWAVTRDIATRLLEYQWNNGIDAGTVGRPDNGM 180
 Db 121 KGNVASTGVSRSEHDTGVSPIAGGYEWAVTRDIATRLLEYQWNNGIDAGTVGRPDNGM 180
 QY 181 LSLGVSYRFGQEDAAFPVAPAPAPEVATKHTFLKSDVLENFKATLKPEQQALDOLY 240
 Db 181 LSLGVSYRFGQEDAAFPVAPAPAPEVATKHTFLKSDVLENFKATLKPEQQALDOLY 240
 QY 241 TQLSNMDPKDGSAVVLYDRIGSEAYNQOLSEKRAQSVDYLVAKGIPAKISARGMGE 300
 Db 241 TQLSNMDPKDGSAVVLYDRIGSEAYNQOLSEKRAQSVDYLVAKGIPAKISARGMGE 300
 QY 301 SNPVGTGNTCDNVKARAALIDCLAPDRREIEVKYKEVVTOPAG 344
 Db 301 SNPVGTGNTCDNVKARAALIDCLAPDRREIEVKYKEVVTOPAG 344

RESULT 10

ARM47796 ID: AAM47796 standard; protein: 344 AA.
 XX AC: AAM47796;

DT 01-MAR-2002 (first entry)

XX DE: Klebsiella pneumoniae OmpA Protein.
 XX KW: enterobacterium; antibacterial; antifungal; antiviral;
 XX antiparasitic; antimicrobial; infection.

OS: Klebsiella pneumoniae.
 XX PN: WO20018326-A1.
 XX PD: 22-NOV-2001.
 XX PF: 16-MAY-2001; 2001WO-FR01490

XX PR: 16-MAY-2000; 2000FR-0006199.
 XX PA: (FABR) FABRE MEDICAMENT SA PIERRE.

XX PI: Jeannin P, Delineste Y, Baussant T;
 XX DR: 2002-055641-07.

XX PT: Use of an enterobacterium OmpA protein for prophylactic and therapeutic treatment of viral, bacterial, fungal and parasitic infections - Claim 8; Page 21-25; 33pp; French.

CC The present sequence is OmpA protein from enterobacteria Klebsiella pneumoniae. OmpA protein can be used to prepare an antimicrobial pharmaceutical composition for mucosal delivery. The composition can be used for prophylactic and therapeutic treatment of viral, bacterial, fungal and parasitic infections.

XX SQ: Sequence 344 AA;
 XX Best Local Similarity 100.0%; Score 344; DB 23; Length 344;
 XX Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKAIFYLNAAPPKDNTWYAGGKLIGSQYHDTGYGNGFQNNGPTRNDQLGAGAFFGGYQVN 60

RESULT 11

AAR93797

ID: AAR93797 standard; protein: 344 AA.

XX AC: AAR93797;

DT 16-SEP-1998 (first entry)

XX DE: Protein LP40, a variant of OmpA protein P40 from K. pneumoniae I-145.
 XX KW: Outer membrane protein; OmpA; P40; immunocomplex; oligosaccharide; polysaccharide; vaccine; Salmonella.
 XX OS: Synthetic.
 OS: Klebsiella pneumoniae.

XX PN: WO9741888-A1.

XX PD: 13-NOV-1997.

XX PF: 06-MAY-1997; 97WO-FR000600.

XX PR: 07-MAY-1996; 96FR-0005592.

XX PA: (FABR) FABRE MEDICAMENT SA PIERRE.
 XX PI: Binz R, Haeuw JF, Svensson S;
 XX WPI: 1997-558694/51.
 XX N-PSSB; AAV13868.

PT: Immunogenic complex for use in anti-bacterial vaccine - comprises bacterial Oligo- or polysaccharide coupled to a Gram-negative bacterial outer membrane protein or a Streptococcal HSA binding protein.

CC The patent discloses a new immunogenic complex which consists of (1) an Oligo- or polysaccharide found naturally on bacteria, coupled to (2) a carrier protein chosen from (a) the human serum albumin binding protein of Streptococcus, (b) Gram-negative bacterial outer membrane proteins (Omp), or (c) fragments of these proteins. The immunogenic complex is useful in vaccines to protect animals against infection by *Salmonella*, especially those belonging to antigenic specificity group O:9, including *S. enteritidis*, *S. panama* and *S. dublin*. A vaccine prepared using an oligosaccharide from *S. enteritidis* can be used to provide protection against septicemia caused by *S. typhi* and against typhoid fever, as well as to protect humans and animals from toxic infections

CC and zoonosis caused by *Salmonella* of the same serogroup; The carrier
 CC proteins enhance the immunogenicity of the Oligo- or polysaccharide
 CC antigens. Inclusion of additional *Salmonella* capsule antigens, such as
 CC the Vi antigen, increases the vaccine's efficacy against encapsulated
 CC bacteria. The present sequence, protein LP40, is a preferred example of
 CC obtained by recombinant which can be used in the immunocomplex. It is
 CC obtained by expression of a modified Kleb. pneumoniae I-145
 XX gene in *E. coli*.

SQ Sequence 344 AA;

Query Match	99.4%	Score 342;	DB 18;	Length 344;
Best Local Similarity	100.0%	Pred. No. 0;	Gaps 0;	
Matches 342;	Conservative 0;	Mismatches 0;	Indels 0;	
Db	1 MKAIFVLAAPKDNNTYAGGLGLWSOYHDGFGYQNGPQNNGPTNDQLAGARGGQYN 60			
Db	1 MKAIFVLAAPKDNNTWAGGLGLWSOYHDGFGYQNGPQNNGPTNDQLAGARGGQYN 60			
Qy	61 PYLGFMEMGYDWLGRMAYKGSVNDGAFAKAQGVQTLAKGYPTTDDIYTRLGGMWRA 120			
Db	61 PYLGFMEMGYDWLGRMAYKGSVNDGAFAKAQGVQTLAKGYPTTDDIYTRLGGMWRA 120			
Qy	121 KGNYASTGVSRSEHTDGTGSVPFAGGVWAVTRDIATRLEYQWNINIDAGTVTRPDNGM 180			
Db	121 KGNYASTGVSRSEHTDGTGSVPFAGGVWAVTRDIATRLEYQWNINIDAGTVTRPDNGM 180			
Qy	181 LSLGVSYRFQEDDAPVVAAPAPAPEVAKHFLKSDVLFENFKENATLKPEGQALDOLY 240			
Db	181 LSLGVSYRFQEDDAPVVAAPAPAPEVAKHFLKSDVLFENFKENATLKPEGQALDOLY 240			
Qy	241 TQLSNMDPKDGSAVVULGYDTRIGSEAYNQLSERKASRAQSIVDLYVAKGIPAGKISARGNGE 300			
Db	241 TQLSNMDPKDGSAVVULGYDTRIGSEAYNQLSERKASRAQSIVDLYVAKGIPAGKISARGNGE 300			
Qy	301 SNPVTGNTCDNVKARAALIDCLAPDRVEIYKGKEVVTQP 342			
Db.	301 SNPVTGNTCDNVKARAALIDCLAPDRVEIYKGKEVVTQP 342			

RESULT 12

ID AAY44077 standard; Protein: 344 AA.
 XX AC AAY44 077;
 XX DT 18-JAN-2000 (first entry)

DE K. pneumoniae OmpA protein.
 XX Outer membrane protein; OmpA; enterobacterium; *Klebsiella pneumoniae*; KW immunity; mammal; antigen; hapten; infection; human; bovine;
 KW respiratory syncytial virus; protective response.
 OS *Klebsiella pneumoniae*.
 PN FR2776521-A1.

XX PD 01-OCT-1999.

XX PF 27-MAR-1998; 98FR-0003814.
 XX PR 27-MAR-1998; 98FR-0003814.

XX PA (FABR) FABRE MEDICAMENT SA PIERRE.
 XX DR WPI; 1999-583089/50.
 XX N-PSDB; AAZ30471.

XX Immunogetic composition containing bacterial outer membrane protein
 conjugated or fused to antigen or hapten, for nasal administration, to
 DE Amino acid sequence of a *Klebsiella* protein.
 XX KW zwitterionic detergent; immune response; vaccine; IgA production;
 KW IgG response; tumour; viral infection; bacterial infection.
 KW Parasitic infection.

XX OS *Klebsiella pneumoniae*.
 XX PN FR2805163-A1.

XX PD 24-AUG-2001..

XX PR 21-FEB-2000; 2000FR-0002104.

XX PR 21-FEB-2000; 2000FR-0002104.

PT protect against respiratory pathogens -
 XX Claim 1; Page 17-18; 64pp; French.
 XX
 CC The invention relates to the use of a fragment of a bacterial membrane
 CC protein, especially the outer membrane protein from an enterobacterium,
 CC e.g. the OmpA protein from *Klebsiella pneumoniae*, in a composition for
 CC nasal administration to improve immunity, in mammals, against an antigen
 CC or hapten. The antigen or hapten is derived from bacteria and viruses
 CC that cause respiratory infections e.g. the human or bovine respiratory
 CC syncytial virus. This sequence corresponds to the OmpA protein from
 CC *Klebsiella*. The antigens are shown in AAY44078-Y44149 (AAZ30478-Z23038
 CC for coding sequences). The use of a membrane protein, from a species
 CC other than that from which the antigen is derived, induces a protective
 CC response against the antigen, even without an adjuvant, since most
 CC adults will already be sensitized against the membrane protein, although
 CC the membrane protein-antigen product will induce an anti-membrane
 CC protein response even in subjects who are not pre-sensitized.
 XX SQ Sequence 344 AA;
 XX Query Match 99.4%; Score 342; DB 20; Length 344;
 XX Best Local Similarity 100.0%; Pred. No. 0; Gaps 0;
 XX Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX Qy 1 MKAIFVLAAPKDNNTWAGGKLGWSQYHDGFGYQNGPQNNGPTNDQLGAGAFGGYQVN 60
 XX Db 1 MKAIFVLAAPKDNNTWAGGKLGWSQYHDGFGYQNGPQNNGPTNDQLGAGAFGGYQVN 60
 XX Qy 61 PYLGFMEMGYDWLGRMAYKGSVNDGAFAKAQGVQTLAKGYPTTDDIYTRLGGMWRA 120
 XX Db 61 PYLGFMEMGYDWLGRMAYKGSVNDGAFAKAQGVQTLAKGYPTTDDIYTRLGGMWRA 120
 XX Qy 121 KGNYASTGVSRSEHTDGTGSVPFAGGVWAVTRDIATRLEYQWNINIDAGTVTRPDNGM 180
 XX Db 121 KGNYASTGVSRSEHTDGTGSVPFAGGVWAVTRDIATRLEYQWNINIDAGTVTRPDNGM 180
 XX Qy 181 LSLGVSYRFQEDDAPVVAAPAPAPEVAKHFLKSDVLFENFKENATLKPEGQALDOLY 240
 XX Db 181 LSLGVSYRFQEDDAPVVAAPAPAPEVAKHFLKSDVLFENFKENATLKPEGQALDOLY 240
 XX Qy 241 TQLSNMDPKDGSAVVULGYDTRIGSEAYNQLSERKASRAQSIVDLYVAKGIPAGKISARGNGE 300
 XX Db 241 TQLSNMDPKDGSAVVULGYDTRIGSEAYNQLSERKASRAQSIVDLYVAKGIPAGKISARGNGE 300
 XX Qy 301 SNPVTGNTCDNVKARAALIDCLAPDRVEIYKGKEVVTQP 342
 XX Db. 301 SNPVTGNTCDNVKARAALIDCLAPDRVEIYKGKEVVTQP 342

XX	(FABR) FABRE MEDICAMENT SA PIERRE.	OS	Klebsiella pneumoniae.
PA		XX	
XX	Goestch L, Corvai N, Beck A, Haeuw JF;	PN	FR2801219-A1.
PI		XX	
XX	WPI; 2001-591759/67.	PD	25-MAY-2001.
DR		XX	
N-PSDB; AAH78461.		PF	18-SEP-2000; 2000FR-0011862.
XX		XX	
PT	Mucosally administered vaccines containing zwitterionic detergents to induce or improve immune response towards antigen or hapten, especially used in antibacterial, antiviral, antiparasitic or antitumor vaccines	PR	27-MAR-1998; 98FR-0003014.
PT		XX	
PT		PA	(FABR) FABRE MEDICAMENT SA PIERRE
PT		XX	
XX		PI	Andreoni C, Rauli I, Nguyen T, Haeuw JF, Baussant T;
PS		XX	
XX	Disclosure: Page 21-22; 26pp; French.	DR	WPI; 2001-358003/38.
CC		DR	N-PSDB; AAF900077.
CC	The present sequence represents a Klebsiella protein. The protein is administered to test the adjuvant effect of zwitterionic detergents.	XX	
CC	The specification describes the use of zwitterionic detergents in the preparation of a mucosally administered pharmaceutical composition for inducing or improving the immune response of a mammal towards an antigen or hapten. In presence of zwitterionic detergents vaccines are effective on mucosal (especially nasal) administration, which has the general advantages of inducing specific IgA production directly at the site of infection, stimulating a systemic IgG-type response (creating a secondary barrier against infection) and being simpler to carry out than administration by injection. The pharmaceutical composition is specifically a vaccine for the treatment or prophylaxis of tumours or viral, bacterial or parasitic infections.	PT	Recombinant production of a protein, for particularly use as a carrier protein in nasal vaccines, comprises renaturation, after extraction, in the presence of specific detergents.
CC		PT	
CC		PT	
CC		PT	
CC		XX	
CC		PS	Claim 8; Page 26-27; 48pp; French.
CC		XX	
CC		CC	The present sequence represents a recombinant outer membrane protein A, designated rp4. The specification describes a method for the recombinant production of a protein, or its fragments. The method comprises renaturation of the protein, after extraction, in the presence of a solution containing one of the detergents zwittergent 3-14, zwittergent 3-12 and octylglucopyranoside, where the protein is not beta-interferon. The protein is especially the outer membrane protein (OMP) from an enterobacterium, and is useful as a carrier for delivering antigens or haptens in a nasal vaccine formulation, particularly directed against pathogens of the respiratory tract, e.g. respiratory syncytial virus (RSV), (para)influenza, hanta virus, streptococci, pneumococci and Meningococci, especially human or bovine RSV. Most adults show an antibody response to the Klebsiella pneumoniae P40, and this sensitisation stimulates the immune response to an antigen/hapten conjugated to the protein.
CC		CC	
CC		CC	
CC		CC	
XX		CC	
SQ	Sequence 344 AA;	XX	
Query	99.4%; Score 342; DB 22; Length 344;	Sequence	344 AA;
Best Local Similarity	100.0%; Pred. No. 0;	Query Match	99.4%; Score 342; DB 22; Length 344;
Matches	342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Best Local Similarity	100.0%; Pred. No. 0;
Qy	1 MKAIFVLNAAPKDNFTWYAGGKLWGSQYHDITGFGYNGFQNNGPTRNDLGAGFGGYQVN 60	Matches	0; Mismatches 0; Indels 0; Gaps 0;
Db	1 MKAIFVLNAAPKDNFTWYAGGKLWGSQYHDITGFGYNGFQNNGPTRNDLGAGFGGYQVN 60	Qy	1 MKAIFVLNAAPKDNFTWYAGGKLWGSQYHDITGFGYNGFQNNGPTRNDLGAGFGGYQVN 60
Qy	61 PYLGFEMGMGYDWLGRHAYKGYSVDNGAKFAQGVQLTAKLGIPITDDLDIYPRGGNWRADS 120	Db	1 MKAIFVLNAAPKDNFTWYAGGKLWGSQYHDITGFGYNGFQNNGPTRNDLGAGFGGYQVN 60
Db	61 PYLGFEMGMGYDWLGRHAYKGYSVDNGAKFAQGVQLTAKLGIPITDDLDIYPRGGNWRADS 120	Qy	1 MKAIFVLNAAPKDNFTWYAGGKLWGSQYHDITGFGYNGFQNNGPTRNDLGAGFGGYQVN 60
Qy	121 KGNYASTGVSRSEHDGTGSEAYNQOLSERAKAQSVDYLAKGIPAKGKSARGMGE 180	Db	1 MKAIFVLNAAPKDNFTWYAGGKLWGSQYHDITGFGYNGFQNNGPTRNDLGAGFGGYQVN 60
Db	121 KGNYASTGVSRSEHDGTGSEAYNQOLSERAKAQSVDYLAKGIPAKGKSARGMGE 180	Qy	61 PYLGFEMGMGYDWLGRHAYKGYSVDNGAKFAQGVQLTAKLGIPITDDLDIYPRGGNWRADS 120
Qy	181 LSLGVSYRFQEDAAPVAPAPAPEAVATKHFILKSDVLFNFKATLKPEGOALDOLY 240	Db	61 PYLGFEMGMGYDWLGRHAYKGYSVDNGAKFAQGVQLTAKLGIPITDDLDIYPRGGNWRADS 120
Db	181 LSLGVSYRFQEDAAPVAPAPAPEAVATKHFILKSDVLFNFKATLKPEGOALDOLY 240	Qy	121 KGNYASTGVSRSEHDGTGSEAYNQOLSERAKAQSVDYLAKGIPAKGKSARGMGE 180
Qy	241 TQLSNMDPKGSQVAVLGYTRIGSEAYNQOLSERAKAQSVDYLAKGIPAKGKSARGMGE 300	Db	121 KGNYASTGVSRSEHDGTGSEAYNQOLSERAKAQSVDYLAKGIPAKGKSARGMGE 180
Db	241 TQLSNMDPKGSQVAVLGYTRIGSEAYNQOLSERAKAQSVDYLAKGIPAKGKSARGMGE 300	Qy	181 LSLGVSYRFQEDAAPVAPAPAPEAVATKHFILKSDVLFNFKATLKPEGOALDOLY 240
Qy	301 SNPVTGNTCDNVKARAALIDCLAPDRRVELEVKGKYKEVYVTP 342	Db	181 LSLGVSYRFQEDAAPVAPAPAPEAVATKHFILKSDVLFNFKATLKPEGOALDOLY 240
Db	301 SNPVTGNTCDNVKARAALIDCLAPDRRVELEVKGKYKEVYVTP 342	Qy	241 TQLSNMDPKGSQVAVLGYTRIGSEAYNQOLSERAKAQSVDYLAKGIPAKGKSARGMGE 300
RESULT 14		Db	241 TQLSNMDPKGSQVAVLGYTRIGSEAYNQOLSERAKAQSVDYLAKGIPAKGKSARGMGE 300
AAB84122	ID AAB84122 standard; Protein: 344 AA.	XX	
XX		AC AAB84122;	
XX		DT 06-AUG-2001 (first entry)	
XX		DE Amino acid sequence of a recombinant outer membrane protein A (rp40).	
XX		KW Outer membrane protein A; rp40; OMP; enterobacterium; nasal vaccine;	
XX		KW respiratory tract pathogen.	

RESULT 15
AAB67771 standard; Protein: 452 AA.
ID AAB67771

AA 452 AA.

XX	AAB67771;	Db	301
XX	SNPTGNTCDNVKARAALIDCLAPDRRVIEVKGYKEVVTQP 342	SNPTGNTCDNVKARAALIDCLAPDRRVIEVKGYKEVVTQP 342	
DT	11-JUN-2001 (first entry)	Search completed: April 15, 2003 , 08:55:13	
DE	Amino acid sequence of a fusion protein of P40 and RSV antigen.	Job time : 64 secs	
XX			
KW	Outer membrane protein A; OmpA; P40; enterobacteria; nasal composition;		
KW	RSV; RSV infection; lung; respiratory tract; vaccine.		
XX			
OS	Synthetic.		
OS	Klebsiella pneumoniae.		
OS	Respiratory syncytial virus.		
PN	WO20021203-A1.		
XX			
PD	29-MAR-2001.		
XX			
PF	22-SEP-2000; 2000WO-FR02626.		
XX			
PR	23-SEP-1999; 99FR-00111888.		
XX			
PA	(FABR) FABRE MEDICAMENT SA PIERRE.		
XX			
PI	Corviale N, Goetsch L;		
XX			
PS	WPI: 2001-257929/26.		
DR	DR-N-PSDD; AF080153.		
XX			
PT	Vaccine against respiratory syncytial virus, comprises enterobacterial outer membrane protein and viral immunogen, provides protective response throughout the respiratory tract		
PT			
PS	Example 2: Page 31-32; 39pp; French.		
XX			
CC	The present sequence represents a fusion protein comprising a Klebsiella pneumoniae outer membrane protein A (OmpA) designated P40 and a respiratory syncytial virus (RSV) antigen. Enterobacterium OmpA proteins, associated with an immunogenic peptide from RSV are used to prepare a nasal composition that induces a protective response, against RSV infection in the upper and lower (lung) respiratory tract. OmpA potentiates the immune response to some immunogenic peptides, eliminating the need for adjuvants. The method is useful for producing vaccines for prevention or treatment of RSV infections.		
XX			
PS	Sequence 452 AA;		
QY	Query Match 99.4%; Score 342; DB 22; Length 452;		
DB	Best Local Similarity 100.0%; Pred. No. 0; Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 MKAIFVLNAAPKDNTWYAGGKLGWSQYHDTGTYGNQFONNNGPTRNDOLGAGAFGGYQVN 60		
DB	1 MKAIFVLNAAPKDNTWYAGGKLGWSQYHDTGTYGNQFONNNGPTRNDOLGAGAFGGYQVN 60		
QY	61 PYLGFEMGYDWLGRMAYKGSDVNDGAFKAQGYOLTAKGYPTDDLDIYTTRIGGMVRADS 120		
DB	61 PYLGFEMGYDWLGRMAYKGSDVNDGAFKAQGYOLTAKGYPTDDLDIYTTRIGGMVRADS 120		
QY	121 KGNVASTGVSRSEHDGTGSPVAGGVENAVTRDIATRLEYQHNNIGDAGTVTRDPNGM 180		
DB	121 KGNVASTGVSRSEHDGTGSPVAGGVENAVTRDIATRLEYQHNNIGDAGTVTRDPNGM 180		
QY	181 LSIGVSYRFQEDAAPVYAAPAPAPEWATKFTLKDVLNFNKATLKPEQQADQLY 240		
DB	181 LSIGVSYRFQEDAAPVYAAPAPAPEWATKFTLKDVLNFNKATLKPEQQADQLY 240		
QY	241 TQLSNMDPKDGSAVLVGLGTDIGSEANQQLSERKRAQSVVDYLVAKGIPAGRISARGMGE 300		
DB	241 TQLSNMDPKDGSAVLVGLGTDIGSEANQQLSERKRAQSVVDYLVAKGIPAGRISARGMGE 300		
QY	301 SNPTGNTCDNVKARAALIDCLAPDRRVIEVKGYKEVVTQP 342		

Result No.	Score	Query	Match	Length	DB ID	Description
SUMMARIES						
1	335	97.4	335	4	US-08-8316-500A-2	Sequence 2, App1
2	179	52.0	179	4	US-08-8316-500A-4	Sequence 4, App1
3	72	20.9	72	4	US-08-8316-500A-6	Sequence 6, App1
4	53	15.4	53	4	US-08-8316-500A-8	Sequence 8, App1
5	10	2.9	359	1	US-08-8316-500A-10	Sequence 10, App1
6	10	2.9	359	3	US-08-8316-722A-2	Sequence 2, App1
7	9	2.6	338	1	US-08-8316-722A-4	Sequence 1, App1
8	9	2.6	594	3	US-08-8316-964-2	Sequence 2, App1
9	9	2.3	26	3	US-08-8316-610-10	Sequence 106, App1
10	8	2.3	100	6	52524666-19	Patent No. 5232466
11	8	2.3	165	1	US-08-8316-70B-106	Sequence 127, App1
12	8	2.3	165	1	US-08-8316-537-106	Sequence 106, App1
13	8	2.3	165	2	US-08-8316-507-106	Sequence 106, App1
14	8	2.3	165	1	US-08-8316-507-106	Sequence 106, App1
15	8	2.3	165	4	US-08-8316-610-10	Sequence 106, App1
16	8	2.3	170	4	US-09-433-043B-106	Sequence 127, App1
17	8	2.3	197	1	US-08-690-995-127	Sequence 1, App1
18	8	2.3	197	3	US-09-113-789-5	Sequence 5, App1
19	8	2.3	404	4	US-09-232-168A-8	Sequence 8, App1
20	8	2.3	498	4	US-09-103-754A-5	Sequence 5, App1
21	8	2.3	537	3	US-08-900-610-2	Sequence 2, App1
22	8	2.3	550	5	PCT-US93-007A-21	Sequence 1, App1
23	8	2.3	719	4	US-08-765-007A-15	Sequence 15, App1
24	8	2.3	805	4	US-09-513-783A-178	Sequence 178, App1
25	7	2.0	35	4	US-09-001-984C-11	Sequence 11, App1
26	7	2.0	35	4	US-09-001-984C-42	Sequence 42, App1
27	7	2.0	40	4	US-08-795-430-4	Sequence 4, App1

28	4	40	4	US-08-510-133A-8	Sequence 8, App1	
29	7	2.0	40	4	US-08-585-995-8	Sequence 4, App1
30	7	2.0	40	4	US-09-355-700-4	Sequence 8, App1
31	7	2.0	59	1	US-08-601-132-8	Sequence 25, App1
32	7	2.0	59	1	US-08-306-871-25	Sequence 6, App1
33	7	2.0	59	1	US-08-565-959-25	Sequence 6, App1
34	7	2.0	61	5	PCT-US92-09419-6	Sequence 6, App1
35	7	2.0	61	5	US-08-094-898-6	Sequence 9, App1
36	7	2.0	67	2	US-08-162-551B-9	Sequence 2, App1
37	7	2.0	95	1	US-08-910-403-2	Sequence 4, App1
38	7	2.0	96	2	US-08-347-492B-4	Sequence 4, App1
39	7	2.0	96	2	US-08-798-143-4	Sequence 2, App1
40	7	2.0	140	2	US-08-001-195-1	Sequence 2, App1
41	7	2.0	169	1	US-07-041-646-9	Sequence 9, App1
42	7	2.0	169	1	US-08-163-823-2	Sequence 2, App1
43	7	2.0	169	1	US-09-179-729B-2	Sequence 2, App1
44	7	2.0	169	2	US-09-996-271-2	Sequence 2, App1
45	7	2.0	169	2	US-08-361-201A-2	Sequence 4, App1
46	7	2.0	140	2	PCT-US5-15-84-4	Sequence 4, App1
47	7	2.0	172	1	US-07-041-146-17	Sequence 17, App1
48	7	2.0	172	1	US-08-147-023-17	Sequence 17, App1
49	7	2.0	169	1	US-08-147-510-17	Sequence 9, App1
50	7	2.0	169	1	US-08-147-570-9	Sequence 9, App1
51	7	2.0	169	2	US-08-449-639A-9	Sequence 9, App1
52	7	2.0	172	1	US-08-141-146-17	Sequence 17, App1
53	7	2.0	172	1	US-08-147-023-17	Sequence 17, App1
54	7	2.0	172	1	US-08-147-510-17	Sequence 9, App1
55	7	2.0	172	2	US-08-149-000-17	Sequence 17, App1
56	7	2.0	182	3	PCT-US92-741B-2	Sequence 2, App1
57	7	2.0	182	4	US-09-160-567-2	Sequence 2, App1
58	7	2.0	270	2	US-07-857-224B-77	Sequence 7, App1
59	7	2.0	270	2	US-07-838-184-3	Sequence 3, App1
60	7	2.0	286	1	US-08-641-646-11	Sequence 4, App1
61	7	2.0	286	4	US-09-132-528-4	Sequence 3, App1
62	7	2.0	286	4	US-08-875-194-3	Sequence 4, App1
63	7	2.0	286	4	US-09-599-366-4	Sequence 3, App1
64	7	2.0	286	4	US-08-875-494-3	Sequence 4, App1
65	7	2.0	286	4	US-08-147-023-11	Sequence 11, App1
66	7	2.0	288	4	US-09-942-985-2	Sequence 2, App1
67	7	2.0	310	1	US-07-841-646-11	Sequence 11, App1
68	7	2.0	317	1	US-08-147-023-11	Sequence 11, App1
69	7	2.0	317	1	US-08-147-023-11	Sequence 11, App1
70	7	2.0	317	1	US-08-147-023-11	Sequence 11, App1
71	7	2.0	317	2	US-08-149-700-11	Sequence 11, App1
72	7	2.0	317	2	US-08-149-700-11	Sequence 11, App1
73	7	2.0	317	2	US-08-449-699A-11	Sequence 11, App1
74	7	2.0	325	1	US-08-382-184-2	Sequence 2, App1
75	7	2.0	325	2	US-08-641-356-2	Sequence 2, App1
76	7	2.0	325	4	US-09-132-528-2	Sequence 2, App1
77	7	2.0	325	4	US-09-132-528-3	Sequence 2, App1
78	7	2.0	325	4	US-08-875-494-3	Sequence 2, App1
79	7	2.0	325	4	US-09-599-366-2	Sequence 2, App1
80	8	2.0	325	4	US-09-599-366-3	Sequence 3, App1
81	7	2.0	325	4	US-08-875-494-2	Sequence 2, App1
82	7	2.0	332	4	US-08-818-1112-53	Sequence 12, App1
83	7	2.0	332	4	US-08-812-1111-53	Sequence 12, App1
84	7	2.0	332	4	US-09-056-556-53	Sequence 18, App1
85	7	2.0	348	4	PCT-US95-04228-18	Sequence 18, App1
86	7	2.0	348	4	US-08-861-464-12	Sequence 21, App1
87	7	2.0	337	2	US-08-237-341-5	Sequence 5, App1
88	7	2.0	337	4	US-09-133-433A-12	Sequence 12, App1
89	7	2.0	348	4	US-08-222-616-18	Sequence 18, App1
90	7	2.0	348	4	US-09-056-648-18	Sequence 18, App1
91	7	2.0	361	4	US-08-874-563B-21	Sequence 21, App1
92	7	2.0	367	1	US-08-841-616-15	Sequence 15, App1
93	7	2.0	408	1	US-08-147-023-15	Sequence 15, App1
94	7	2.0	408	1	US-08-149-700-15	Sequence 15, App1
95	7	2.0	419	1	US-07-141-666-19	Sequence 19, App1
96	7	2.0	419	1	US-08-147-023-19	Sequence 19, App1

101	2.0	419	1	US-08-447-570-19	Sequence 19, App1	1.7	30	1	US-08-447-570-19	Sequence 12, App1	
102	7	419	2	US-08-449-700-19	Sequence 19, App1	1.7	30	1	US-08-449-700-19	Sequence 14, App1	
103	7	419	2	US-08-449-699A-19	Sequence 19, App1	1.7	30	2	US-08-449-699A-19	Sequence 14, App1	
104	7	421	4	US-09-020-846-68	Sequence 68, App1	1.7	30	4	US-08-462-211A-14	Sequence 14, App1	
105	7	2.0	428	4	US-09-139-064-4	Sequence 2, App1	1.7	31	1	US-08-460-874A-12	Sequence 12, App1
106	7	2.0	428	4	US-09-139-064-4	Sequence 4, App1	1.7	31	1	US-08-460-874A-12	Sequence 13, App1
107	7	2.0	428	4	US-09-139-064-4	Sequence 2, App1	1.7	31	2	US-08-460-874A-13	Sequence 12, App1
108	7	2.0	428	4	US-09-139-064-4	Sequence 4, App1	1.7	31	2	US-08-460-874A-13	Sequence 13, App1
109	10.0	433	1	US-08-810-116-9	Sequence 9, App1	1.7	31	2	US-08-388-883B-13	Sequence 12, App1	
110	7	2.0	433	2	US-07-930-548A-9	Sequence 9, App1	1.7	31	4	US-08-462-211A-12	Sequence 13, App1
111	7	2.0	437	1	US-08-810-116-10	Sequence 10, App1	1.7	32	1	US-08-388-883B-15	Sequence 13, App1
112	7	2.0	437	2	US-07-930-548A-10	Sequence 10, App1	1.7	32	1	US-08-388-883B-15	Sequence 15, App1
113	7	2.0	484	1	US-07-841-1646-3	Sequence 13, App1	1.7	32	4	US-08-388-883B-15	Sequence 15, App1
114	7	2.0	484	1	US-08-147-370-4	Sequence 4, App1	1.7	32	4	US-08-388-883B-15	Sequence 15, App1
115	7	2.0	484	1	US-08-147-370-4	Sequence 4, App1	1.7	32	4	US-08-388-883B-15	Sequence 15, App1
116	7	2.0	484	2	US-08-449-700-13	Sequence 13, App1	1.7	32	4	US-08-388-883B-15	Sequence 15, App1
117	7	2.0	484	2	US-08-449-699A-13	Sequence 13, App1	1.7	32	4	US-08-388-883B-15	Sequence 15, App1
118	7	2.0	582	3	US-08-906-8865-3	Sequence 3, App1	1.7	32	4	US-08-388-883B-15	Sequence 15, App1
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651	6	US-08-993-722A-76	Sequence 76, App1
652	6	US-08-993-722A-78	Sequence 78, App1
653	6	US-08-993-722A-80	Sequence 80, App1
654	6	US-08-993-722A-82	Sequence 82, App1
655	6	US-08-993-722A-84	Sequence 84, App1
656	6	US-08-993-722A-86	Sequence 86, App1
657	6	US-08-993-722A-88	Sequence 88, App1
658	6	US-08-993-722A-90	Sequence 90, App1
659	6	US-08-993-722A-92	Sequence 92, App1
660	6	US-08-993-722A-94	Sequence 94, App1
661	6	US-08-993-722A-96	Sequence 96, App1
662	6	US-08-993-722A-98	Sequence 98, App1
663	6	US-08-993-722A-100	Sequence 100, App1
664	6	US-08-993-722A-112	Sequence 112, App1
665	6	US-08-993-722A-114	Sequence 114, App1
666	6	US-08-993-722A-116	Sequence 116, App1
667	6	US-08-993-722A-118	Sequence 118, App1
668	6	US-08-993-722A-120	Sequence 120, App1
669	6	US-08-993-722A-122	Sequence 122, App1
670	6	US-08-993-722A-124	Sequence 124, App1
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672	6	US-08-993-722A-128	Sequence 128, App1
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674	6	US-08-993-722A-132	Sequence 132, App1
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676	6	US-08-993-722A-136	Sequence 136, App1
677	6	US-08-993-722A-138	Sequence 138, App1
678	6	US-08-993-722A-140	Sequence 140, App1
679	6	US-08-993-722A-142	Sequence 142, App1
680	6	US-08-993-722A-144	Sequence 144, App1
681	6	US-08-993-722A-146	Sequence 146, App1
682	6	US-08-993-722A-148	Sequence 148, App1
683	6	US-08-993-722A-150	Sequence 150, App1
684	6	US-08-993-722A-152	Sequence 152, App1

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833	4	US-08-940-086A-11	Sequence 11, App1
834	4	US-08-935-105A-11	Sequence 11, App1
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865	5	US-08-766-598A-4	Sequence 25, App1
866	5	US-09-174-060-25	Sequence 25, App1
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876	5	US-08-646-981-2	Sequence 67, App1
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878	5	US-08-340-283-120	Sequence 6, App1
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930	5	US-08-934-297-53	Sequence 53, App1
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933	5	US-07-933-321-64	Sequence 63, App1
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974	5	US-09-160-513-29	Sequence 41, App1
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976	5	US-08-408-858A-5	Sequence 5, App1

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979	2	1.5	US-08-945-168-93	Sequence 93, AppI
980	3	1.5	US-08-946-141A-16	Sequence 26, AppI
981	4	1.5	US-09-561-490E-9	Sequence 9, AppI
982	5	1.5	PCT-1595-13794-26	Sequence 26, AppI
983	5	1.5	US-08-481-658B-16	Sequence 16, AppI
984	6	1.5	US-08-477-504A-16	Sequence 16, AppI
985	6	1.5	US-08-486-756A-16	Sequence 16, AppI
986	6	1.5	US-08-945-168-12	Sequence 92, AppI
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989	6	1.5	US-08-487-077A-16	Sequence 16, AppI
990	6	1.5	US-08-485-863A-16	Sequence 16, AppI
991	6	1.5	US-09-171-705-33	Sequence 33, AppI
992	6	1.5	US-09-171-705-34	Sequence 34, AppI
993	6	1.5	US-09-485-049D-16	Sequence 16, AppI
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99998	5	1.5	US-07-838-450-20	Sequence 20, AppI
99999	5	1.5	US-08-471-791-6	Sequence 6, AppI
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ALIGNMENTS

JU DNVKARALIDCLAPDRVIEVKYKEVVTQPG 344
 JU DNV-836-500A-2
 sequence 2, Application US/08836500A
 GENERAL INFORMATION:
 APPLICANT: Blinz, Hans
 APPLICANT: Bauscant, Thierry
 APPLICANT: Haew, Jean-Francois
 APPLICANT: Nguyen Ngoc, Thien
 TITLE OF INVENTION: Carrier Protein Having an Adjuvant Effect, Immunogenic Complex Containing It, Process for Their Preparation, Nucleotide Sequence and Vaccines
 TITLE OF INVENTION: Effect, Immunogenic Complex Containing It, Process for Their Preparation, Nucleotide Sequence and Vaccines
 Patent No. 6197929
 NUMBER OF SEQUENCES: 8
 ADDRESSSEE: Rockey, Milnamow & Katz, Ltd.
 STREET: 180 N. Stetson, 2 Prudential Plaza, Suite 4700
 CITY: Chicago
 STATE: Illinois
 COUNTRY: U.S.A.
 ZIP: 60601
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/836,500A
 FILING DATE:
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: Katz, Martin L.
 REGISTRATION NUMBER: 25,011
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312-616-5400
 TELEFAX: 312-616-5460
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 335 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 RESULT 2
 US-08-836-500A-4
 Sequence 4, Application US/08836500A
 Patent No. 6197929
 GENERAL INFORMATION:
 APPLICANT: Blinz, Hans
 APPLICANT: Bauscant, Thierry
 APPLICANT: Haew, Jean-Francois
 APPLICANT: Nguyen Ngoc, Thien
 TITLE OF INVENTION: Carrier Protein Having an Adjuvant Effect, Immunogenic Complex Containing It, Process for Their Preparation, Nucleotide Sequence and Vaccines
 Patent No. 6197929
 NUMBER OF SEQUENCES: 8
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Rockey, Milnamow & Katz, Ltd.
 STREET: 180 N. Stetson, 2 Prudential Plaza, Suite 4700
 CITY: Chicago
 STATE: Illinois
 COUNTRY: U.S.A.
 ZIP: 60601
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/836,500A
 FILING DATE:
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: Katz, Martin L.
 REGISTRATION NUMBER: 25,011
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312-616-5400
 TELEFAX: 312-616-5460
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 179 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein

; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-036-500A-4

Query Match Score 52.0%; Score 179; DB 4; Length 179;
Best Local Similarity 100.0%; Pred. No. 5.4e-158;
Matches 179; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 4
US-08-436-500A-8
Sequence 8, Application US/08836500A
Patent No. 6197929
GENERAL INFORMATION:
APPLICANT: Baulant, Thierry
APPLICANT: Baulant, Hans
APPLICANT: Haewiu, Jean-Francois
APPLICANT: Nguyen Ngoc, Thien
TITLE OF INVENTION: Carrier Protein Having an Adjuvant
TITLE OF INVENTION: Effect, Immunogenic Complex Containing It, Process for
TITLE OF INVENTION: Their Preparation, Nucleotide Sequence and Vaccines
Patent No. 6197929

NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rockey, Milnamow & Katz, Ltd.
Patent No. 6197929
GENERAL INFORMATION:
APPLICANT: Baulant, Thierry
APPLICANT: Haewiu, Jean-Francois
APPLICANT: Nguyen Ngoc, Thien
TITLE OF INVENTION: Carrier Protein Having an Adjuvant
TITLE OF INVENTION: Effect, Immunogenic Complex Containing It, Process for
TITLE OF INVENTION: Their Preparation, Nucleotide Sequence and Vaccines
Patent No. 6197929

NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rockey, Milnamow & Katz, Ltd.
STREET: 180 N. Stetson, 2 Prudential Plaza, Suite
STREET: 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/836,500A
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Katz, Martin L.
REGISTRATION NUMBER: 25,011
REFERENCE/DOCKET NUMBER: PIE1514P0180US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 53 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-836-500A-8

RESULT 5
US-08-457-997B-2
Sequence 2, Application US/08457997B
Patent No. 576608
GENERAL INFORMATION:
APPLICANT: Kolattukudy, P. E.
TITLE OF INVENTION: Otitis Media Vaccine
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Calfee, Halter and Griswold
STREET: Suite 1800 800 Superior Avenue

Query Match Score 20.9%; Score 72; DB 4; Length 72;
Best Local Similarity 100.0%; Pred. No. 2.3e-59;
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 5
US-08-457-997B-2
Sequence 2, Application US/08457997B
Patent No. 576608
GENERAL INFORMATION:
APPLICANT: Kolattukudy, P. E.
TITLE OF INVENTION: Otitis Media Vaccine
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Calfee, Halter and Griswold
STREET: Suite 1800 800 Superior Avenue

Query Match Score 136; DB 4; Length 188
Best Local Similarity 100.0%; Pred. No. 1.1e-51;
Matches 136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match Score 176; DB 4; Length 176
Best Local Similarity 100.0%; Pred. No. 1.1e-51;
Matches 176; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CITY: Cleveland
 STATE: Ohio
 COUNTRY: U.S.A.
 ZIP: 44114-2688

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/457,997B
 FILING DATE:
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: Golrick, Mary E.
 REGISTRATION NUMBER: 34,829
 REFERENCE/DOCKET NUMBER: 22727/00102
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (216) 622-8458
 TELEFAX: (216) 241-0816

INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 359 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein

US-08-457-997B-2

RESULT 6
 US-08-467-722A-2
 Sequence 2, Application US/08467722A
 Pat No. 6030526

GENERAL INFORMATION:
 APPLICANT: Kolattukudy, P. E.
 TITLE OF INVENTION: Otitis Media Vaccine
 NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Calfee, Halter and Griswold
 STREET: Suite 1800, 800 Superior Avenue
 CITY: Cleveland
 STATE: Ohio
 COUNTRY: U.S.A.
 ZIP: 44114-2688

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/467,722A
 FILING DATE:
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: Golrick, Mary E.
 REGISTRATION NUMBER: 34,829
 REFERENCE/DOCKET NUMBER: 22727/00102
 TELEPHONE: (216) 622-8458
 TELEFAX: (216) 241-0816

INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 359 amino acids
 TYPE: amino acid
 TOPOLOGY: linear

Query Match 2.9%; Score 10; DB 1; Length 359;
 Best Local Similarity 100.0%; Pred. No. 0.19; Mismatches 0; Indels 0; Gaps 0;

Qy 321 CLAPDRVEI 330
 Db 344 CLAPDRVEI 353

RESULT 7
 US-08-210-394-1
 Sequence 1, Application US/08210394
 Pat No. 5770213

GENERAL INFORMATION:
 APPLICANT: Zlotnick Dr., Gary W.
 TITLE OF INVENTION: Purified No. 5770213typable Haemophilus influenzae p5 Protein as a Vaccine for No. 5770213typable Haemophilus influenzae Strain

NUMBER OF SEQUENCES: 1

CORRESPONDENCE ADDRESS:
 ADDRESSEE: American Cyanamid Company
 STREET: One Cyanamid Plaza
 CITY: Wayne
 STATE: New Jersey
 COUNTRY: US

21P: 07470-8426

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/210,394
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: Harrington, James J.
 REFERENCE/DOCKET NUMBER: 32,144
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 201/831-3246
 TELEFAX: 201/831-3305

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
 LENGTH: 338 amino acids
 TYPE: amino acid
 STRANDEDNESS: unknown
 TOPOLOGY: unknown
 MOLECULE TYPE: protein

US-08-210-394-1

Query Match 2.8%; Score 9; DB 1; Length 338;
 Best Local Similarity 100.0%; Pred. No. 1.6; Mismatches 0; Indels 0; Gaps 0;

Qy 322 LAPDRVEI 330
 Db 324 LAPDRVEI 332

RESULT 8
 US-08-826-964-2
 Sequence 2, Application US/08826964
 Pat No. 603663

GENERAL INFORMATION:
 APPLICANT: Ketcham, Catherine M.
 TITLE OF INVENTION: Nucleic Acids Encoding GDP-Fucose Pyrophosphorylase

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend and Crew LLP

Tue Apr 15 09:25:24 2003

us-09-831-061-2.oligo.rai

STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
GENERAL INFORMATION:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/8226,964.
FILING DATE: 09-APR-1997
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 60/015,241
FILING DATE: 10-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REG-STRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 014137-009910US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 594 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
us-08-8226-964-2

Query Match 2.6%; Score 9; DB 3; Length 594;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 9
us-08-920-610-10
/ Sequence 10, Application US/08920610
/ Patent No. 6015709
GENERAL INFORMATION:
APPLICANT: Natesan, Sridaran
TITLE OF INVENTION: TRANSCRIPTIONAL ACTIVATORS, AND
TITLE OF INVENTION: COMPOSITIONS AND USES RELATED THERETO
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, HOG & ELIOT LLP
STREET: One Post Office Square
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109-2170

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/920,610
FILING DATE: 27-AUG-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: APV-006.02
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-832-1000
TELEFAX: 617-832-7000

; INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-920-610-10
Query Match 2.3%; Score 8; DB 3; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 199 APAPAPAP 206
Db 16 APAPAPAP 23
RESULT 10
5252466-19
; Patent No. 5252466
; APPLICANT: CROMAN, JOHN E.
; TITLE OF INVENTION: FUSION PROTEINS HAVING A SITE FOR IN
; VIVO POST-TRANSLATION MODIFICATION AND METHODS OF MAKING AND
; PURIFYING THEM
; NUMBER OF SEQUENCES: 24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/525,568
; FILING DATE: 18-MAY-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 354,266
; FILING DATE: 19-MAY-1989
; SEQ ID NO:19:
; LENGTH: 100
; 5252466-19
Query Match 2.3%; Score 8; DB 6; Length 100;
Best Local Similarity 100.0%; Pred. No. 4.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 199 APAPAPAP 206
Db 9 APAPAPAP 16
RESULT 11
US-07-956-700B-106
/ Sequence 106, Application US/07956700B
/ Patent No. 5539002
GENERAL INFORMATION:
; APPLICANT: Robert Haselkorn and Piotr Gornicki
; TITLE OF INVENTION: Cyanobacterial and Plant Acetyl-CoA
; NUMBER OF SEQUENCES: 116
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: 321 No. 553902nd Clark Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60610
COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII-DOS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/956,700B
; FILING DATE: 19921002
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Thomas E. No. 5539092thrup
; REGISTRATION NUMBER: 33,268

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; REFERENCE/DOCKET NUMBER: ARCD:058
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 1-312-744-0090
; INFORMATION FOR SEQ ID NO: 106:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 165 amino acids
; TYPE: Amino acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; MOLECULE TYPE: Peptide
; US-07-956-700B-106

Query Match 2.3% Score 8; DB 1; Length 165;
Best Local Similarity 100.0%; Pred. No. 7.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 199 APAPAPAP 206
Db 74 APAPAPAP 81

; RESULT 12
; US-08-476-537-106
; Sequence 106, Application US/08476537
; Patent No. 5756590
; GENERAL INFORMATION:
; APPLICANT: Robert Haselkorn and Piotr Gornicki
; TITLE OF INVENTION: Cyanobacterial and Plant Acetyl-CoA
; NUMBER OF SEQUENCES: 116
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: 321 No. 5792627th Clark Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60610
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII-DOS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US-08/485,607
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/956,700
; FILING DATE: 10/21/92
; ATTORNEY/AGENT INFORMATION:
; NAME: Thomas E. No. 5792627thrup
; REGISTRATION NUMBER: 33,268
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 1-312-744-0090
; TELEFAX: 1-312-755-4489
; INFORMATION FOR SEQ ID NO: 106:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 165 amino acids
; TYPE: Amino acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; MOLECULE TYPE: Peptide
; US-08-485-607-106

Query Match 2.3% Score 8; DB 1; Length 165;
Best Local Similarity 100.0%; Pred. No. 7.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 199 APAPAPAP 206
Db 74 APAPAPAP 81

; RESULT 14
; US-08-475-879-106
; Sequence 106, Application US/08475879
; Patent No. 5972644
; LENGTH: 165 amino acids
; TYPE: Amino acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; MOLECULE TYPE: Peptide
; US-08-476-537-106

Query Match 2.3% Score 8; DB 1; Length 165;
Best Local Similarity 100.0%; Pred. No. 7.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 199 APAPAPAP 206
Db 74 APAPAPAP 81

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; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII-DOS
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; APPLICATION NUMBER: US/08/475, 879
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 536
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 07/956,700
; FILING DATE: 10/21/92
; ATTORNEY/AGENT INFORMATION:
; NAME: Thomas E. NO. 597644 5786170thrup
; REGISTRATION NUMBER: 33.268
; REFERENCE/DOCKET NUMBER: ARCD:058
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 1-312-744-0090
; TELEFAX: 1-312-755-4489
; INFORMATION FOR SEQ ID NO: 106:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 165 amino acids
; TYPE: Amino acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; MOLECULE TYPE: Peptide
US-08-475-879-106

Query Match          2.3%; Score 8; DB 2; Length: 165;
Best Local Similarity 100.0%; Pred. No. 7.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   199 APAPAPAP 206
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Db   74 APAPAPAP 81

RESULT 15
US-09-433-043B-106
; Sequence 1.06, Application US/09433043B
; PATENT NO. 639342
; GENERAL INFORMATION:
; APPLICANT: HASELKORN, ROBERT
; APPLICANT: GORNICKI, PIOTR
; TITLE OF INVENTION: CYANOBACTERIAL AND PLANT ACETYL-COA CARBOXYLASE
; FILE REFERENCE: ARCD:338US
; CURRENT APPLICATION NUMBER: US/09433.043B
; CURRENT FILING DATE: 1999-10-25
; PRIOR APPLICATION NUMBER: 08/475,879
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 07/956,700
; PRIOR FILING DATE: 1992-10-02
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 106
; LENGTH: 165
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-433-043B-106

Query Match          2.3%; Score 8; DB 4; Length 165;
Best Local Similarity 100.0%; Pred. No. 7.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   199 APAPAPAP 206
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Db   74 APAPAPAP 81

Search completed: April 15, 2003, 08:56:53
Job time : 30 secs

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Sequence 7, Appl1	US-09-779-666-9
Sequence 19, Appl1	US-09-833-723-19
Sequence 9, Appl1	US-09-734-522-19
Sequence 34, Appl1	US-10-044-703-34
Sequence 62, Appl1	US-10-033-741-62
Sequence 25, Appl1	US-09-839-666-9
Sequence 34, Appl1	US-10-024-123-40
Sequence 9, Appl1	US-09-903-412-9
Sequence 308, App	US-09-966-262-308
Sequence 9, Appl1	US-10-211-069-9
Sequence 2862, App	US-09-880-748-2862
Sequence 308, App	US-09-983-966-308
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Sequence 16, Appl1	US-09-879-333-34
Sequence 40, Appl1	US-09-902-123-40
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Sequence 7, Appl1	US-09-916-201-7
Sequence 16, Appl1	US-09-772-719-16
Sequence 34508, A	US-09-804-761-34508
Sequence 16, Appl1	US-09-984-245-308
Sequence 7, Appl1	US-09-988-842-7
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Sequence 33, Appl1	US-10-038-612-34
Sequence 11, Appl1	US-10-038-612-151
Sequence 15, App	US-10-044-703-22
Sequence 22, Appl1	US-09-880-505-4
Sequence 13, Appl1	US-09-880-505-13
Sequence 3, Appl1	US-09-775-925-3
Sequence 17, Appl1	US-09-925-422-17
Sequence 9, Appl1	US-09-349-755-9
Sequence 13, Appl1	US-09-755-731-18
Sequence 35, Appl1	US-09-349-755-35
Sequence 9, Appl1	US-09-166-334-16
Sequence 16, Appl1	US-09-166-334-35
Sequence 35, Appl1	US-09-555-731-18
Sequence 18, Appl1	US-09-752-724-9
Sequence 9, Appl1	US-09-752-724-10
Sequence 10, Appl1	US-09-752-724-10

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836	25	10	US-09-276-600-9	Sequence 53, App1
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80	1.5	5	US-09-744-869-898	Sequence 898, App1
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RESULT 1
US-10-169-953-2
Sequence 2, Application US/10163953
GENERAL INFORMATION:
APPLICANT: Thierry BAUSSANT
APPLICANT: Pascale JEANNIN
APPLICANT: Yves DELNESTE
APPLICANT: Francois LANNY
APPLICANT: Jean-Yves BONNEFOY
TITLE OF INVENTION: METHOD FOR PREPARING A POLYPEPTIDE SOLUBLE IN AN AQUEOUS SOLVENT
TITLE OF INVENTION: IN THE ABSENCE OF DETERGENT
FILE REFERENCE: D18190
CURRENT APPLICATION NUMBER: US/10/169,953
CURRENT FILING DATE: 2002-07-03
PRIOR APPLICATION NUMBER: FR 00 000070
PRIOR FILING DATE: 2000-01-04
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2

Length: 344
TYPE: PRT
ORGANISM: Klebsiella pneumoniae
FEATURE:
OTHER INFORMATION: P40

Query Match 100.0%; Score 344; DB 9; Length 344;
Best Local Similarity 100.0%; Pred. No. 1..le-18; Mismatches 0; Indels 0; Gaps 0;

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Qy 61 PYLGFMGYDWLGRMAYKGSDNGAFAKQGQYLTAKLGYPITDDIYTRGGMWRADS 120

RESULT 2
US-09-905-176-22
Sequence 22, Application US/09905176
PATENT NO. US2002015906A1
GENERAL INFORMATION:
APPLICANT: CALIFORNIA INSTITUTE OF TECHNOLOGY
APPLICANT: Derek A. DEE
TITLE OF INVENTION: METHOD FOR DETERMINING THREE-DIMENSIONAL PROTEIN STRUCTURE FROM PROTEIN SEQUENCE
FILE REFERENCE: 265/297
CURRENT APPLICATION NUMBER: US/09/905,176
CURRENT FILING DATE: 2002-04-05
PRIOR APPLICATION NUMBER: US 60/218,016
PRIOR FILING DATE: 2000-07-12
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn version 3.1
SEQ ID NO 22
LENGTH: 153
TYPE: PRT
ORGANISM: Escherichia coli
US-09-905-176-22

Query Match 9.6%; Score 33; DB 10; Length 153;
Best Local Similarity 100.0%; Pred. No. 1..e-23; Mismatches 0; Indels 0; Gaps 0;

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DB 56 KAQQVOLTAKLGYPITDDIYTRGGMWRAD 88

RESULT 3
US-09-922-199A-15
Sequence 15, Application US/09922199A
Publication No. US20020187136A1
GENERAL INFORMATION:
APPLICANT: Meyers, Rachel
TITLE OF INVENTION: 15368, A NOVEL HUMAN GTP-RELEASING FACTOR FAMILY MEMBER AND USES THEREFOR
FILE REFERENCE: 381552002500
CURRENT APPLICATION NUMBER: US/09/922,199A
CURRENT FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: 60/222,622
NUMBER OF SEQ ID NOS: 28
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 15
LENGTH: 25
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Consensus amino acid sequence
US-09-922-199A-15

Query Match 2.3%; Score 8; DB 9; Length 25;
 Best Local Similarity 100.0%; Pred. No. 1.1;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 200 PAPAPE 207
 Db 2 PAPAPE 9

RESULT 4
 US-09-864-761-38830
 ; Sequence 38830, Application US/09864761
 ; Patent No. US20048763A1

GENERAL INFORMATION:
 APPLICANT: Penn, Sharron G.
 APPLICANT: Rank, David R.
 APPLICANT: Hanzel, David K.
 APPLICANT: Chen, Wensheng

TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR FILE REFERENCE: Aeonlica X-1

CURRENT FILING DATE: 2001-05-23
 CURRENT APPLICATION NUMBER: US/09/864-761

PRIOR APPLICATION NUMBER: US 60/180, 312
 PRIOR FILING DATE: 2000-02-04

PRIOR APPLICATION NUMBER: US 60/207, 456
 PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: US 09/632, 366
 PRIOR FILING DATE: 2000-08-03

PRIOR APPLICATION NUMBER: GB 24263.6
 PRIOR FILING DATE: 2000-10-04

PRIOR APPLICATION NUMBER: US 60/236, 359
 PRIOR FILING DATE: 2000-09-27

PRIOR APPLICATION NUMBER: PCT/US01/00566
 PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00667
 PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00664
 PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00663
 PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00662
 PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00661
 PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00670
 PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: US 60/234, 687
 PRIOR FILING DATE: 2000-09-21

PRIOR APPLICATION NUMBER: US 09/608, 408
 PRIOR FILING DATE: 2000-06-30

PRIOR APPLICATION NUMBER: US 09/774, 203
 PRIOR FILING DATE: 2001-01-29

NUMBER OF SEQ ID NOS: 49117

SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
 SEQ ID NO 38830
 LENGTH: 60

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.6
 OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3
 OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.2
 OTHER INFORMATION: SWISSPROT HIT: P55194, EVALUE 3.10e-01

Query Match 2.3%; Score 8; DB 10; Length 60;
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Qy 199 APAPAPAP 206
 Db 40 APAPAPAP 47

RESULT 5
 US-09-922-199A-14
 ; Sequence 14, Application US/09922199A
 ; Publication No US2002187138A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Meyers, Rachael
 ; TITLE OF INVENTION: 15168, A NOVEL HUMAN GTP-RELEASING
 ; FEATURE:
 ; TITLE OF INVENTION: FACTOR FAMILY MEMBER AND USES THEREFOR
 ; FILE REFERENCE: 381552002500
 ; CURRENT APPLICATION NUMBER: US/09/922,199A
 ; CURRENT FILING DATE: 2001-08-02
 ; PRIOR APPLICATION NUMBER: 60/222,622
 ; PRIOR FILING DATE: 2000-08-02
 ; NUMBER OF SEQ ID NOS: 28
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 14
 ; LENGTH: 66
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Consensus amino acid sequence
 US-09-922-199A-14

Query Match 2.3%; Score 8; DB 9; Length 66;
 Best Local Similarity 100.0%; Pred. No. 2.6;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 200 PAPAPE 207
 Db 2 PAPAPE 9

RESULT 6
 US-09-738-626-3880
 ; Sequence 3880, Application US/09738626
 ; Publication No. US200219765A1
 ; GENERAL INFORMATION:
 ; APPLICANT: NAKAGAWA, SATOSHI
 ; APPLICANT: MIZOGUCHI, HIROSHI
 ; APPLICANT: ANDO, SEIKO
 ; APPLICANT: HAYASHI, MIKIRO
 ; APPLICANT: OCHIBI, KEIKO
 ; APPLICANT: YOKOI, HARUHIKO
 ; APPLICANT: TATEISHI, NAOKO
 ; APPLICANT: SENOH, AKIHIRO
 ; APPLICANT: IKEDA, MASATO
 ; APPLICANT: OZAKI, AKIO
 ; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
 ; FILE REFERENCE: 749-125
 ; CURRENT APPLICATION NUMBER: US/09/738, 626
 ; CURRENT FILING DATE: 2000-12-18
 ; PRIOR APPLICATION NUMBER: JP 99/377484
 ; PRIOR FILING DATE: 1999-12-16
 ; PRIOR APPLICATION NUMBER: JP 00/159162
 ; PRIOR FILING DATE: 2000-04-07
 ; PRIOR APPLICATION NUMBER: JP 00/280988
 ; PRIOR FILING DATE: 2000-08-03
 ; NUMBER OF SEQ ID NOS: 7059

OTHER INFORMATION: MAP TO Z83844.5
 OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.9
 OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.3
 OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.5
 OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 5
 OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3.7

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; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 3880
; LENGTH: 191
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
us-09-738-626-3880

Query Match Score 8; DB 9; Length 191;
Best Local Similarity 100.0%; Pred. No. 6.7;
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Qy 199 APAPAPAP 206
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RESULT 9
us-09-965-703-54
; Sequence 54, Application US/09965703
; Patent No. US20020119521A1
; GENERAL INFORMATION:
; APPLICANT: Rohm and Haas Company
; APPLICANT: Palli, Subba Reddy
; APPLICANT: Kapitskaya, Marianna Zinovjevna
; APPLICANT: Cress, Dean Ervin
; TITLE OF INVENTION: NO. US20020119521A1: Ecdysone Receptor-Based Inducible Gene Express
; FILE REFERENCE: A01020B
; CURRENT APPLICATION NUMBER: US/09/965,703
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/191,355
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 60/269,799
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: PCT/US01/09050
; PRIOR FILING DATE: 2001-03-21
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 54
; LENGTH: 269
; ORGANISM: Homo sapiens
us-09-965-703-54

Query Match Score 8; DB 10; Length 269;
Best Local Similarity 100.0%; Pred. No. 9.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 199 APAPAPAP 206
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Db 108 APPAPAPAP 115

RESULT 9
us-10-042-417-50
; Sequence 50, Application US/10042417
; Patent No. US200213082A1
; GENERAL INFORMATION:
; APPLICANT: Pagano, M.
; TITLE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT OF
; PROLIFERATIVE AND DIFFERENTIATIVE DISORDERS
; FILE REFERENCE: 5914-090 999
; CURRENT APPLICATION NUMBER: US/10/042,417
; CURRENT FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: 60/260,179
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 50
; LENGTH: 283
; TYPE: PRT
; ORGANISM: Homo sapiens
us-10-042-417-50

Query Match Score 8; DB 9; Length 283;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 199 APAPAPAP 206

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Db 261 ||||| 268
; APPLICANT: LEVINE, et al.
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
; FILE REFERENCE: 802620-2005.1
; CURRENT APPLICATION NUMBER: US/09/771.161A
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/724, 676
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 136776
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 135619
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 273
; LENGTH: 547
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-771-161A-273

Query Match
Best Local Similarity 100.0%; Pred. No. 17;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Score 8; DB 10; Length 547;

Qy 199 APAPAPAP 206
Db 42 APAPAPAP 49

RESULT 13
US-09-298-523B-63
; Sequence 63, Application US/09298523B
; Publication No. US20030059438A1
; GENERAL INFORMATION:
; APPLICANT: BRILES, et al.
; TITLE OF INVENTION: PNEUMOCOCCAL SURFACE PROTEIN C (PSPC), EPITOPIC REGIONS
; FILE REFERENCE: 454312-3140
; CURRENT APPLICATION NUMBER: US/09/298,523B
; CURRENT FILING DATE: 1999-04-23
; NUMBER OF SEQ ID NOS: 78
; SEQ ID NO: 63
; SOFTWARE: PatentIn Ver. 2.1
; LENGTH: 670
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
; US-09-298-523B-63

Query Match
Best Local Similarity 100.0%; Pred. No. 17;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Score 8; DB 9; Length 670;

Qy 199 APAPAPAP 206
Db 42 APAPAPAP 49

RESULT 14
US-09-298-523B-62
; Sequence 62, Application US/09298523B
; Publication No. US20030059438A1
; GENERAL INFORMATION:
; APPLICANT: BRILES, et al.
; TITLE OF INVENTION: PNEUMOCOCCAL SURFACE PROTEIN C (PSPC), EPITOPIC REGIONS
; FILE REFERENCE: 454312-3140
; CURRENT APPLICATION NUMBER: US/09/298,523B
; CURRENT FILING DATE: 1999-04-23
; NUMBER OF SEQ ID NOS: 78
; SEQ ID NO: 62
; LENGTH: 701
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
; US-09-771-161A-272

Query Match
Best Local Similarity 100.0%; Pred. No. 17;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Score 8; DB 9; Length 547;

Qy 199 APAPAPAP 206
Db 42 APAPAPAP 49

RESULT 12
US-09-771-161A-273
; Sequence 273, Application US/09771161A
; Publication No. US2002010811A1
; GENERAL INFORMATION:

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US-09-298-523B-62

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 Best Local Similarity 100.0%; Pred. No. 22;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 200 PAPAPAPE 207
 Db 646 PAPAPAPE 653

RESULT 15

US-09-298-523B-2
 Sequence 2, Application US/09298523B
 Publication No. US20030059438A1
 GENERAL INFORMATION:
 APPLICANT: BRILES et al.
 TITLE OF INVENTION: PNEUMOCOCCAL SURFACE PROTEIN C (PSPC), EPITOPIIC REGIONS
 TITLE OF INVENTION, AND STRAINS THEREOF AND USES THEREFOR
 FILE REFERENCE: 454312-3140
 CURRENT APPLICATION NUMBER: US/09/298-523B
 CURRENT FILING DATE: 1999-04-23
 NUMBER OF SEQ ID NOS: 78
 SOFTWARE: Patentin Ver. 2.1
 SEQ ID NO 2
 LENGTH: 707
 TYPE: PRT
 ORGANISM: Streptococcus pneumoniae
 us-09-298-523B-2

Query Match 2.3%; Score 8; DB 9; Length 707;
 Best Local Similarity 100.0%; Pred. No. 22;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 200 PAPAPAPE 207
 Db 647 PAPAPAPE 654

Search Completed: April 15, 2003, 09:03:33
 Job time : 38 secs

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107	7	14	variant-specific s	2	JQ1438	
108	7	14	microtubule-associ	2	S39866	
109	7	14	trip operon leader	2	A87933	
110	7	14	trip operon leader	2	C65203	
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112	7	66	trip operon leader	2	argininosuccinate	
113	7	66	hypothetical 7.7K	2	argininosuccinate	
114	7	105	metallothionein ol	2	probable arginos	
115	7	108	H71635	cell division prot	2	polypeptide - tuli
116	7	120	C72451	outer membrane pro	2	outer membrane pro
117	7	120	AF1646	tein B0205_10 [2	protein B0205_10 [
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119	7	129	D51844	argininosuccinate	2	argininosuccinate
120	7	132	I63131	centromere/microtu	2	argininosuccinate
121	7	138	S52933	synapsin IIB - hum	2	probable arginos
122	7	155	E64105	probable integral	2	polypeptide - hum
123	7	171	B96548	transcription init	2	probable arginos
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125	7	200	C84631	probable PPE prote	2	protein - hum
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128	7	210	A43696	heat shock transcr	2	protein - hum
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136	7	246	T03931	probable protein K	2	protein - hum
137	7	246	H96711	probable protein K	2	protein - hum
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253	1087	2	T30844	serine-repeat anti	326	6	1.7	G75265
254	1095	1	A31225	phospholipase C (E	327	6	1.7	A29349
255	1111	2	T29070	hypothetical prote	328	6	1.7	AG2003
256	1123	2	A44766	defective chorion-	329	6	1.7	A71530
257	1125	1	F70177	transcription repa	330	6	1.7	H81684
258	1131	2	S2266	FUN30 protein - Ye	331	6	1.7	F70585
259	1132	2	C75259	probable iron-sulf	332	6	1.7	S65804
260	1147	1	MWAXIB	myosin heavy chain	333	6	1.7	A84613
261	1149	2	T27567	hypothetical prote	334	6	1.7	AG1195
262	1239	1	Q0BE10	BOLFI Protein - hu	335	6	1.7	T11229
263	1274	0	S55050	cardiac myosin-bin	336	6	1.7	T42978
264	1298	2	A48999	protein-tirosine k	337	6	1.7	136
265	1323	2	E88257	protein let-23 [im	338	6	1.7	130
266	1374	2	S70712	protein-tirosine k	339	6	1.7	AE1324
267	1464	2	S58984	developmental prote	340	6	1.7	138
268	1487	1	EDBEE1	immediate-early pr	341	6	1.7	H70784
269	1487	1	EDBEF6	155K transcriptio	342	6	1.7	140
270	1589	2	C44766	defective chorion-	343	6	1.7	S74072
271	1618	2	S21424	-nésin - human	344	6	1.7	B69515
272	2156	1	RRVUNE	genome polyprotein	345	6	1.7	B82783
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274	2510	2	T51023	hypothetical prote	347	6	1.7	T31442
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278	6	1.7	S77777	n	351	6	1.7	139
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294	6	1.7	89	hypothetical prote	367	6	1.7	153
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298	6	1.7	92	p10 - Orgy	371	6	1.7	157
299	6	1.7	94	phosphocarrier Pro	372	6	1.7	158
300	6	1.7	95	cuticule Protein Lm	373	6	1.7	159
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302	6	1.7	100	probable glycine-r	375	6	1.7	161
303	6	1.7	104	conserved hypothet	376	6	1.7	162
304	6	1.7	104	p10 protein - Orny	377	6	1.7	163
305	6	1.7	108	hypothetical prote	378	6	1.7	164
306	6	1.7	108	hypothetical prote	379	6	1.7	165
307	6	1.7	113	conserved hypothet	380	6	1.7	166
308	6	1.7	115	ribosomal protein	381	6	1.7	167
309	6	1.7	115	V2 protein - tomat	382	6	1.7	168
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311	6	1.7	118	hypothetical prote	384	6	1.7	170
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409	6	T36207	482	6	1.7	227	2	E8907
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422	6	CB9601	495	6	1.7	233	2	F9816
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435	6	F75468	508	6	1.7	244	2	T20810
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437	6	CB9601	510	6	1.7	244	2	T16942
438	6	A41275	511	6	1.7	245	2	G64834
439	6	AH337	512	6	1.7	245	2	A2195
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445	6	F75468	518	6	1.7	250	2	F83604
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452	6	CB9601	525	6	1.7	256	2	T36161
453	6	A41275	526	6	1.7	256	2	T25073
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455	6	F75468	528	6	1.7	255	2	AB2109
456	6	D70017	529	6	1.7	258	2	G96023
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460	6	F75468	533	6	1.7	259	2	AC0332
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463	6	A41275	536	6	1.7	259	2	probable surface protein
464	6	AH337	537	6	1.7	259	2	heat-labile enteric
465	6	F75468	538	6	1.7	259	2	hypothetical protein
466	6	D70017	539	6	1.7	261	2	probable OmpA fami
467	6	CB9601	540	6	1.7	262	2	AF2698

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553	6	1.7	267	2	C90411	6	1.7	B75509	
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556	6	1.7	268	2	F64024	6	1.7	616	2
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558	6	1.7	269	2	H75576	6	1.7	617	2
559	6	1.7	269	2	T28957	6	1.7	617	2
560	6	1.7	271	2	C69407	6	1.7	617	2
561	6	1.7	272	2	T35961	6	1.7	617	2
562	6	1.7	272	2	F64024	6	1.7	622	2
563	6	1.7	273	2	T30959	6	1.7	623	2
564	6	1.7	273	2	T1630	6	1.7	624	2
565	6	1.7	274	2	T47937	6	1.7	624	2
566	6	1.7	275	2	G75606	6	1.7	625	2
567	6	1.7	276	1	A65077	6	1.7	625	2
568	6	1.7	276	2	T35961	6	1.7	625	2
569	6	1.7	276	2	F64024	6	1.7	626	2
570	6	1.7	276	2	C92273	6	1.7	628	2
571	6	1.7	276	2	S22274	6	1.7	629	2
572	6	1.7	277	2	AG2295	6	1.7	630	2
573	6	1.7	277	2	G71849	6	1.7	631	2
574	6	1.7	277	2	S71222	6	1.7	631	2
575	6	1.7	278	2	H82488	6	1.7	631	2
576	6	1.7	278	2	B45247	6	1.7	641	2
577	6	1.7	279	2	C69112	6	1.7	642	2
578	6	1.7	279	2	E69226	6	1.7	643	2
579	6	1.7	280	2	F97024	6	1.7	644	2
580	6	1.7	280	2	G84636	6	1.7	645	2
581	6	1.7	280	2	D84968	6	1.7	646	2
582	6	1.7	281	2	H70942	6	1.7	647	2
583	6	1.7	281	2	S78161	6	1.7	648	2
584	6	1.7	282	2	J00115	6	1.7	649	2
585	6	1.7	282	2	A99205	6	1.7	650	2
586	6	1.7	283	2	A82310	6	1.7	651	2
587	6	1.7	283	2	G88349	6	1.7	652	2
588	6	1.7	283	2	E88597	6	1.7	653	2
589	6	1.7	283	2	T27027	6	1.7	654	2
590	6	1.7	284	2	AC2551	6	1.7	655	2
591	6	1.7	284	2	D32354	6	1.7	656	2
592	6	1.7	285	2	G69204	6	1.7	657	2
593	6	1.7	285	2	E40590	6	1.7	658	2
594	6	1.7	285	2	F71076	6	1.7	659	2
595	6	1.7	285	2	S30557	6	1.7	660	2
596	6	1.7	285	2	S38806	6	1.7	661	2
597	6	1.7	285	2	S07193	6	1.7	662	2
598	6	1.7	285	2	AE2006	6	1.7	663	2
599	6	1.7	285	2	T02543	6	1.7	668	2
600	6	1.7	285	2	F82338	6	1.7	669	2
601	6	1.7	285	2	T35270	6	1.7	670	2
602	6	1.7	285	2	T87072	6	1.7	671	2
603	6	1.7	285	2	F97480	6	1.7	672	2
604	6	1.7	285	2	S09209	6	1.7	673	2
605	6	1.7	285	2	H72278	6	1.7	674	2
606	6	1.7	285	2	T44617	6	1.7	675	2
607	6	1.7	285	2	D70314	6	1.7	676	2
608	6	1.7	285	2	S55063	6	1.7	677	2
609	6	1.7	285	2	C8787	6	1.7	678	2
610	6	1.7	285	2	F81325	6	1.7	679	2
611	6	1.7	298	2	F97463	6	1.7	680	2
612	6	1.7	298	2	C8787	6	1.7	681	2
613	6	1.7	298	2	F81325	6	1.7	682	2

687	2	S40853	probable porin precursor	2-keto-3-deoxy-D-galactone-3-kinase	S20736	1.7	357	2
688	6	C86080	probable GDSL-motif protein	F3H9.6	T00578	1.7	358	2
689	6	C91233	outer membrane protein	-	B86409	1.7	359	2
690	6	B95114	conserved hypothetical protein	-	S17456	1.7	360	2
691	6	G90884	probable UDP-GalacNac beta-mannosidase	763	6	1.7	360	2
692	6	B85930	probable UDP-GalacNac beta-mannosidase	764	6	1.7	360	2
693	6	E70384	biotin synthase [stage V sporulation]	765	6	1.7	360	2
694	6	B82607	hypothetical protein	766	6	1.7	360	2
695	6	T23840	conserved hypothetical protein	767	6	1.7	360	2
696	6	B96532	hypothetical protein	768	6	1.7	362	2
697	6	D71655	hypothetical protein	769	6	1.7	362	2
698	6	B90442	mannan endo-1,4-beta-D-glucuronidase	770	6	1.7	362	2
699	6	D83842	trNA (uracil-5')-tRNA cyclohydrolase	771	6	1.7	363	2
700	6	T33457	hypothetical protein	772	6	1.7	364	2
701	6	T16330	hypothetical protein	773	6	1.7	364	2
702	6	JC4102	hypothetical protein	774	6	1.7	364	2
703	6	DE2YG3	hypothetical protein	775	6	1.7	364	2
704	6	S36824	glyceraldehyde-3-phosphate dehydrogenase	776	6	1.7	365	2
705	6	D83201	beta-D-galactoside a-	777	6	1.7	365	2
706	6	JC7712	probable glycosyltransferase	778	6	1.7	365	2
707	6	T2399	hypothetical protein	779	6	1.7	366	2
708	6	154229	hypothetical protein	780	6	1.7	366	2
709	6	T20807	hypothetical protein	781	6	1.7	367	2
710	6	AD3252	urodoporphyrinogen III polymerase	782	6	1.7	367	2
711	6	A12760	DNA polymerase III protein FIN19.3	783	6	1.7	367	2
712	6	E966668	[1] Gal beta 1,3GalNAc	784	6	1.7	367	2
713	6	A45073	hypothetical protein	785	6	1.7	367	2
714	6	T02399	hypothetical protein	786	6	1.7	367	2
715	6	B72507	hypothetical protein	787	6	1.7	371	2
716	6	VABPA7	major capsid protein	788	6	1.7	371	2
717	6	B75274	conserved hypothetical protein	789	6	1.7	371	2
718	6	S72475	glucanase (EC 3.2.1.7)	790	6	1.7	371	2
719	6	A2B260	probable L-lactate sulfite reductase	791	6	1.7	373	2
720	6	E72005	sulfite reductase	792	6	1.7	373	2
721	6	A43815	transforming protein	793	6	1.7	374	2
722	6	G83171	hypothetical protein	794	6	1.7	374	2
723	6	B75274	conserved hypothetical protein	795	6	1.7	374	2
724	6	S57338	probable ABC transporter	796	6	1.7	374	2
725	6	D98170	probable ABC transporter	797	6	1.7	375	2
726	6	A22780	probable ABC transporter	798	6	1.7	375	2
727	6	JC7188	probable ABC transporter	799	6	1.7	375	2
728	6	F97169	probable ABC transporter	800	6	1.7	376	2
729	6	H86558	probable ABC transporter	801	6	1.7	376	2
730	6	I39355	probable ABC transporter	802	6	1.7	376	2
731	6	A22780	probable ABC transporter	803	6	1.7	376	2
732	6	A85531	probable ABC transporter	804	6	1.7	376	2
733	6	E90680	probable ABC transporter	805	6	1.7	376	2
734	6	FMSP32	probable ABC transporter	806	6	1.7	377	2
735	6	E71373	probable ABC transporter	807	6	1.7	377	2
736	6	G97541	DNA polymerase III	808	6	1.7	378	2
737	6	T23369	hypothetical protein	809	6	1.7	378	2
738	6	FMSX3N	photosystem II protein	810	6	1.7	378	2
739	6	FMNT32	photosystem II protein	811	6	1.7	378	2
740	6	FMSY32	photosystem II protein	812	6	1.7	378	2
741	6	FMRZ32	photosystem II protein	813	6	1.7	378	2
742	6	EMNT3D	photosystem II protein	814	6	1.7	379	2
743	6	F2WDW1	photosystem II protein	815	6	1.7	379	2
744	6	F2CN1U	photosystem II protein	816	6	1.7	380	2
745	6	F2PMD1	photosystem II protein	817	6	1.7	380	2
746	6	F2NT1C	photosystem II protein	818	6	1.7	380	2
747	6	F2KMLM	photosystem II protein	819	6	1.7	381	2
748	6	A21730	photosystem II protein	820	6	1.7	381	2
749	6	A5579	photosystem II protein	821	6	1.7	382	2
750	6	S18555	photosystem II protein	822	6	1.7	382	2
751	6	S33912	photosystem II protein	823	6	1.7	383	1
752	6	S57265	photosystem II protein	824	6	1.7	383	1
753	6	S42492	photosystem II protein	825	6	1.7	383	2
754	6	H83462	hypothetical protein	826	6	1.7	383	2
755	6	F83914	dihydrotaempferol	827	6	1.7	383	2
756	6	T48619	glycerol-3-phosphate acyl transferase	828	6	1.7	383	2
757	6	S41265	cell division protein	829	6	1.7	383	2
758	6	D48376	poly(3-hydroxybutyrate)	830	6	1.7	384	2
759	6	S29214	hypothetical protein	831	6	1.7	384	2
		F83914	hypothetical protein	832	6	1.7	384	2

833	2	T22678	906	6	1.7	410	2	C868335
834	2	E83491	907	6	1.7	411	2	S153333
835	2	S74778	908	6	1.7	411	2	A70509
836	6	1.7	386	2	B75616	909	6	1.7
837	6	1.7	386	2	F83994	910	6	1.7
838	6	1.7	388	2	S34672	911	6	1.7
839	6	1.7	388	2	S76932	912	6	1.7
840	6	1.7	389	1	SAVLAH	913	6	1.7
841	6	1.7	389	1	SAVLBH	914	6	1.7
842	6	1.7	389	1	SAVLAJ	915	6	1.7
843	6	1.7	389	1	SAVLAI	916	6	1.7
844	6	1.7	389	1	SAVLCP	917	6	1.7
845	6	1.7	389	2	S41871	918	6	1.7
846	6	1.7	389	2	S47407	919	6	1.7
847	6	1.7	389	2	S32202	920	6	1.7
848	6	1.7	389	2	S20745	921	6	1.7
849	6	1.7	389	2	S20753	922	6	1.7
850	6	1.7	389	2	S20749	923	6	1.7
851	6	1.7	389	2	B75363	924	6	1.7
852	6	1.7	389	2	B96635	925	6	1.7
853	6	1.7	389	2	I49640	926	6	1.7
854	6	1.7	389	2	G70120	927	6	1.7
855	6	1.7	389	2	F75411	928	6	1.7
856	6	1.7	390	1	DNMS53	929	6	1.7
857	6	1.7	390	1	S58814	930	6	1.7
858	6	1.7	390	2	T40497	931	6	1.7
859	6	1.7	390	2	A98336	932	6	1.7
860	6	1.7	390	2	A12946	933	6	1.7
861	6	1.7	390	2	J50296	934	6	1.7
862	6	1.7	390	2	S44285	935	6	1.7
863	6	1.7	391	2	C84268	936	6	1.7
864	6	1.7	391	2	T34935	937	6	1.7
865	6	1.7	393	1	DNHU53	938	6	1.7
866	6	1.7	393	1	S06594	939	6	1.7
867	6	1.7	393	1	F82852	940	6	1.7
868	6	1.7	393	2	C83155	941	6	1.7
869	6	1.7	394	2	T51494	942	6	1.7
870	6	1.7	395	2	AD2119	943	6	1.7
871	6	1.7	395	2	T48301	944	6	1.7
872	6	1.7	395	2	F82852	945	6	1.7
873	6	1.7	396	2	B39170	946	6	1.7
874	6	1.7	396	2	S31959	947	6	1.7
875	6	1.7	396	2	A91019	948	6	1.7
876	6	1.7	396	2	C85863	949	6	1.7
877	6	1.7	397	2	S20617	950	6	1.7
878	6	1.7	398	1	VBBPA7	951	6	1.7
879	6	1.7	398	1	S23351	952	6	1.7
880	6	1.7	398	2	A64882	953	6	1.7
881	6	1.7	398	2	S76788	954	6	1.7
882	6	1.7	399	1	OHSPAD	955	6	1.7
883	6	1.7	399	2	S24959	956	6	1.7
884	6	1.7	399	2	HB3711	957	6	1.7
885	6	1.7	400	1	SAVIA	958	6	1.7
886	6	1.7	401	1	A36361	959	6	1.7
887	6	1.7	401	2	E84869	960	6	1.7
888	6	1.7	401	2	S76788	961	6	1.7
889	6	1.7	401	2	S45583	962	6	1.7
890	6	1.7	401	2	A4488	963	6	1.7
891	6	1.7	401	2	S33334	964	6	1.7
892	6	1.7	402	2	AD1417	965	6	1.7
893	6	1.7	402	2	AF1792	966	6	1.7
894	6	1.7	402	2	JH0403	967	6	1.7
900	6	1.7	402	2	F90035	968	6	1.7
901	6	1.7	403	2	S73773	969	6	1.7
902	6	1.7	403	2	C83977	970	6	1.7
903	6	1.7	403	2	S02709	971	6	1.7
904	6	1.7	403	2	B10659	972	6	1.7
905	6	1.7	404	2	E53097	973	6	1.7
906	6	1.7	404	2	S71264	974	6	1.7
907	6	1.7	404	2	A4488	975	6	1.7
908	6	1.7	404	2	E96958	976	6	1.7
909	6	1.7	404	2	T20847	977	6	1.7
910	6	1.7	404	2	T8726	978	6	1.7
911	6	1.7	404	2	I50689	979	6	1.7

ALIGNMENT S

F_98-109/Region: alanine/proline-rich

Query Match Score 53; DB 2; Length 238;
Best Local Similarity 100.0%; Pred. No. 8e-46;
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 213 FTLKSDVLFENFKATLKPEGQQLDQLYTOQLSNDMPKDGSAVVLGYTDRIGSE 265
Db 116 FTLKSDVLFENFKATLKPEGQQLDQLYTOQLSNDMPKDGSAVVLGYTDRIGSE 168

RESULT 3
S07222 outer membrane protein ompA precursor - Enterobacter aerogenes
C;Species: Enterobacter aerogenes
C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 20-Aug-1993
C;Accession: S07222
R;Braun, G.; Cole, S.T.
Eur. J. Biochem. 137, 495-500, 1983
A;Title: Molecular characterization of the gene coding for major outer membrane protein
A;Reference number: S07222; MUID:84108348; PMID:6363039
A;Molecule type: DNA
A;Residues: 1-350

A;Cross references: EMBL:X00254; NID:940837; PID:CAA25062.1; PID:940838
A;Note: the authors translated the codon CAG for residue 197 as Arg
C;Genetics:
A;Gene: ompA
C;Suppartium: outer membrane protein A
C;Keywords: membrane protein
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-350/Product: outer membrane protein ompA #status predicted <OMPA>
F:213-350/Domain: periplasmic #status predicted <PER>

Query Match Score 53; DB 2; Length 350;
Best Local Similarity 100.0%; Pred. No. 1.1e-45;
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 213 FTLKSDVLFENFKATLKPEGQQLDQLYTOQLSNDMPKDGSAVVLGYTDRIGSE 265
Db 219 FTLKSDVLFENFKATLKPEGQQLDQLYTOQLSNDMPKDGSAVVLGYTDRIGSE 271

RESULT 4
I40703 outer membrane protein A - Citrobacter freundii (fragment)
N;Alternative names: Outer membrane protein II
C;Species: Citrobacter freundii

CDNVKAALIDCLAPDRRVEIEVKGYKEVTTQPA 343
VSRSEHDGTGSPVAGGVWMAVTRDIATRLEYQWNNNIDAGTYGTRPDNGMLSIGVSYR 188
141 VSRSEHDGTGSPVAGGVWMAVTRDIATRLEYQWNNNIDAGTYGTRPDNGMLSIGVSYR 200
189 FGQDAAPVVAAPAPAPAEVATHKFTLKSDFLVNFENFKATLKPEGQQLDQLYTOQLSNMDP 248
201 FGQDAAPVVAAPAPAPAEVATHKFTLKSDFLVNFENFKATLKPEGQQLDQLYTOQLSNMDP 260
249 KDSAVVLYGTDIGSEAYNQOOLESEKRAQSYVDYLVAKGIPACKISARGMGEENPVTGNT 308
261 KDSAVVLYGTDIGSEAYNQOOLESEKRAQSYVDYLVARKGIPACKISARGMGEENPVTGNT 320

C;Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 20-Aug-1999
 C;Accession: I40703
 R;Lawrence, J.G.; Ochman, H.; Hartl, D.L.
 J;Gen. Microbiol. 137, 1911-1921, 1991
 A;Title: Molecular and evolutionary relationships among enteric bacteria.
 A;Reference number: I40701; MUID:92065252; PMID:1955870
 A;Status: preliminary; translated from GB/EMBL/DDJB
 A;Molecule type: DNA
 A;Residues: 1-28 <RES>
 A;Cross-references: GB:M63354; NID:9144441; PIDN:AAA23095.1; PID:9144442
 C;Genetics:
 C;Superfamily: outer membrane protein A
 C;Keywords: membrane protein
 F;99-109/Region: alanine/proline-rich
 Query Match 12.5%; Score 43; DB 2; Length 238;
 Best Local Similarity 100.0%; Pred. No. 1.2e-35;
 Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 292 KISARGMGESENPTCDNVKARALIDCLAPDRVEIEVKG 334
 Db 195 KISARGMGESENPTCDNVKARALIDCLAPDRVEIEVKG 237

RESULT 5
 MMECA
 Outer membrane protein A precursor - Escherichia coli (strain K-12)

N;Alternate names: outer membrane protein II*
 C;Species: Escherichia coli
 C;Date: 30-Sep-1980 #sequence_revision 30-Sep-1980 #text_change 01-Mar-2002
 R;Accession: A93707; A92862; A93855; S50909; D64836; A03434
 R;Beck, E.; Bremer, E.
 Nucleic Acids Res. 8, 3011-3024, 1980
 A;Title: Nucleotide sequence of the gene ompA coding the outer membrane protein II of Escherichia coli. N.I.: Yasunaga, T.; Makino, K.; Ohnishi, K.; Yokoyama, K.; Han, C.; Gotoh, N.; Shingawa, H.
 A;Accession: A93707; MUID:81053729; PMID:6253901
 A;Molecule type: DNA
 A;Residues: 1-346 <BEC>
 A;Cross-references: GB:V00307; GB:J01654; NID:942159; PIDN:CAA23588.1; PID:942161
 R;Novva, N.R.; Nakamura, K.; Inouye, M.
 J. Mol. Biol. 13, 317-328, 1980
 A;Title: Gene structure of the OmpA protein, a major surface protein of Escherichia coli.
 A;Reference number: A92862; MUID:81170587; PMID:6260561
 A;Accession: A92862
 A;Molecule type: DNA
 A;Residues: 1-346 <MOVY>
 A;Experimental source: strain K12

R;Chen, R.; Schmidmayr, W.; Kramer, C.; Chen-Schmeisser, U.; Henning, U.
 Proc. Natl. Acad. Sci. U.S.A. 77, 4592-4596, 1980
 A;Title: Primary structure of major outer membrane protein II* (ompA protein) of Escherichia coli.
 A;Reference number: A93855; MUID:81054820; PMID:7001461
 A;Accession: A93855
 A;Molecule type: protein
 A;Residues: 1-346 <CHPS>
 R;Ruhn, A.; Klefer, D.; Kohne, C.; Zhu, H.Y.; Tschantz, W.R.; Dalbey, R.E.
 Eur. J. Biochem. 226, 891-897, 1994
 A;Title: Evidence for a loop-like insertion mechanism of pro-omp A into the inner membrane.
 A;Reference number: S50909; MUID:9512855; PMID:7813480
 A;Accession: S50909
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-46 <KUH>

A;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cole, S.A.; Rose, D.J.; Mau, B.; Shao, Y.
 Science 277, 1453-1462, 1997
 A;Title: The complete genome sequence of Escherichia coli K-12.
 A;Reference number: A64720; MUID:97426617; PMID:9278503
 A;Accession: D64836

A;Status: nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-346 <BLAT>
 A;Cross-references: GB:AE000198; GB:U00096; NID:91787189; PIDN: AAC74043.1; PID:917871
 A;Experimental source: strain K-12, substrate MG1655
 C;Genetics:
 A;Gene: ompA; tolG; tut; con
 A;Map position: 22 min
 C;Function:
 A;Description: required for the action of colicins K and L and for the stabilization diffusion channels that allow penetration of various solutes
 C;Superfamily: outer membrane protein A
 C;Keywords: membrane protein; monomer
 F;1-21/Domain: signal sequence #status predicted <SIG>
 F;22-146/Domain: outer membrane protein A #status predicted <MAT>
 F;22-196/Domain: intramembrane #status predicted <INT>
 F;196-208/Region: alanine/proline-rich
 F;209-346/Domain: periplasmic #status predicted <PER>
 F;257-301/Domain: ompA-like domain #status predicted <OMP>
 Query Match 9.6%; Score 33; DB 1; Length 346;
 Best Local Similarity 100.0%; Pred. No. 2.6e-25;
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 87 KAQGVQLTAKLGYPTDDIYTRUGMWRAD 119
 Db 94 KAQGVQLTAKLGYPTDDIYTRUGMWRAD 126

RESULT 6
 A90759
 Outer membrane protein 3a [imported] - Escherichia coli (strain O157:H7, substrain EC)
 C;Species: Escherichia coli
 C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 01-Mar-2002
 R;Hayashi, T.; Makino, K.; Kurokawa, K.; Ohnishi, K.; Yokoyama, K.; Han, C.; Gotoh, N.; Yasunaga, T.; Muhara, S.; Shiba, T.; Hattori, M.; Shingawa, H.
 DNA Res. 8, 11-22, 2001
 A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and giga-
 A;Reference number: A996229; MUID:21156331; PMID:11258796
 A;Accession: A90759
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-346 <HAY>
 A;Cross-references: GB:BA000007; PIDN:BAB34464.1; PID:913360501; GSPDB:GN00154
 C;Genetics:
 A;Gene: Ecs1041
 C;Superfamily: outer membrane protein A

Query Match 9.6%; Score 33; DB 2; Length 346;
 Best Local Similarity 100.0%; Pred. No. 2.6e-25;
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 87 KAQGVQLTAKLGYPTDDIYTRUGMWRAD 119
 Db 94 KAQGVQLTAKLGYPTDDIYTRUGMWRAD 126

RESULT 7
 G85622
 Outer membrane protein 3a [imported] - Escherichia coli (strain O157:H7, substrain EC)
 C;Species: Escherichia coli
 C;Accession: G85622
 R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimaranta, E.; Potamousis, K.; Apode
 Nature 409, 529-533, 2001
 A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
 A;Reference number: A85480; MUID:21074935; PMID:11206551
 A;Accession: G85622
 A;Status: preliminary
 A;Molecule type: DNA

A; Residues: 1-346 <STR>
 A; Cross-references: GB:AE005174; NID:912514142; PIDN:AAG55443.1; GSPDB:GN00145; UWGP:213
 C; Genomics:
 A; Gene: ompA
 C; Superfamily: outer membrane protein A
 C; Keywords: outer membrane protein A
 F; 104-115/Region: alanine/proline-rich

Query Match 9.6%; Score 33; DB 2; Length 346;
 Best Local Similarity 100.0%; Pred. No. 2.6e-25;
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 87 KAQQVOLTAKLGYPTDDLDIYTRGGMWRAD 119
 Db 94 KAQQVOLTAKLGYPTDDLDIYTRGGMWRAD 126

RESULT 8
 I62393
 outer membrane protein ompA - Escherichia vulneris (ATCC 33822) (fragment)
 N; Alternative names: Outer membrane protein II
 C; Species: Escherichia vulneris
 A; Variety: ATCC 33822
 C; Date: 04-Sep-1997 #sequence_revision 07-Nov-1997 #text_change 20-Aug-1999
 C; Accession: I62393
 R; Lawrence, J.G.; Ochman, H.; Hartl, D.L.
 J. Gen. Microbiol. 137, 1911-1921, 1991
 A; Title: Molecular and evolutionary relationships among enteric bacteria.
 A; Reference number: I40701; MUID:92065252; PMID:1955870
 A; Accession: I62396
 A; Status: preliminary; translated from GB/EMBL/DDBJ
 A; Molecule type: DNA
 A; Residues: 1-243 <RES>
 A; Cross-references: GB:M63346; NID:9146986; PIDN:AAA24234.1; PID:9146987
 A; Accession: I62390
 A; Status: preliminary; translated from GB/EMBL/DDBJ
 A; Molecule type: DNA
 A; Residues: 1-243 <RES>
 A; Cross-references: GB:M63347; NID:9146994; PIDN:AAA24238.1; PID:9146995
 A; Experimental source: ATCC 3652
 C; Genetics:

A; Gene: ompA
 C; Superfamily: outer membrane protein A
 C; Keywords: outer membrane protein A
 F; 104-115/Region: alanine/proline-rich

Query Match 8.4%; Score 29; DB 2; Length 243;
 Best Local Similarity 100.0%; Pred. No. 2.3e-21;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 210 TKHFTLKSVDLFNFNKATLKPEQQALDQ 238
 Db 118 TKHFTLKSVDLFNFNKATLKPEQQALDQ 146

RESULT 9
 I84331
 outer membrane protein A - Escherichia fergusonii (ATCC 35469) (fragment)
 N; Alternative names: Outer membrane protein II
 C; Species: Escherichia fergusonii
 A; Variety: ATCC 35469
 C; Accession: I84331
 R; Lawrence, J.G.; Ochman, H.; Hartl, D.L.
 J. Gen. Microbiol. 137, 1911-1921, 1991
 A; Title: Molecular and evolutionary relationships among enteric bacteria.
 A; Reference number: I40701; MUID:92065252; PMID:1955870
 A; Accession: I84331
 A; Status: preliminary; translated from GB/EMBL/DDBJ
 A; Molecule type: DNA
 A; Residues: 1-243 <RES>
 A; Cross-references: GB:M63351; NID:9146982; PIDN:AAA24232.1; PID:9146983
 A; Experimental source: ATCC 35469
 C; Genetics:

A; Gene: ompA
 C; Superfamily: outer membrane protein A
 C; Keywords: outer membrane protein A
 F; 103-114/Region: alanine/proline-rich

Query Match 7.8%; Score 27; DB 2; Length 243;
 Best Local Similarity 100.0%; Pred. No. 2.3e-19;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 12	Qy 93 LTAKLGYPIITDDLDIYTRGGMWRAD 119 Db 1 LTAKLGYPIITDDLDIYTRGGMWRAD 27	MMEBAD outer membrane protein A - Escherichia fergusonii (ATCC 35472) (fragment) N;Alternate names: outer membrane protein II C;Species: Escherichia fergusonii A;Variety: ATCC 35472 C;Date: 04-Sep-1997 #sequence_revision 07-Nov-1997 #text_change 04-Mar-2000 C;Accession: I62392; R: Lawrence, J.G.; Ochman, H.; Hartl, D.L. J. Gen. Microbiol. 137, 1911-1921, 1991 A;Title: Molecular and evolutionary relationships among enteric bacteria. A;Reference number: I40701; MUID:92005252; PMID:1955870 A;Accession: I62388 A;Status: preliminary; translated from GB/EMBL/DBBJ A;Molecule type: DNA A;Residues: 1-243 <RES> A;Cross-references: GB:M63352; PIDN:9146990; PIDN:AAA24236.1; PID:9146991 A;Experimental source: ATCC 35471 A;Accession: I62392 A;Status: preliminary; translated from GB/EMBL/DBBJ A;Molecule type: DNA A;Residues: 1-243 <RES> A;Cross-references: GB:M63353; PIDN:9146998; PIDN:AAA24240.1; PID:9146999 A;Experimental source: ATCC 35472 C;Genetics: A;Gene: ompA C;Superfamily: outer membrane protein A C;Keywords: membrane protein A F;103-114/Region: alanine/proline-rich	Query Match Score 7.8%; Score 27; DB 2; Length 243; Best Local Similarity 100.0%; Pred. No. 2.5e-19; Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Qy 93 LTAKLGYPIITDDLDIYTRGGMWRAD 119 Db 1 LTAKLGYPIITDDLDIYTRGGMWRAD 27
RESULT 13		MMEBAD outer membrane protein A precursor - Shigella dysenteriae C;Species: Shigella dysenteriae C;Accession: I62392; R: Braun, G.; Cole, S.T.; Parkhill, J.; Dougan, G.; James, K.D.; Pickard, D.; Wain, J.; Church, T.; Connor, P.; Croplin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Parr, S.; Moule, S.; O'Gaora, P. Nature 413, 848-852, 2001 A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, A;Title: Complete genome sequence of a multiple drug resistant <i>Salmonella enterica</i> serovar Typhi C;Accession: AB05026 A;Accession: AI0626 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-350 <PAR> A;Cross-references: GB:AL513382; PIDN:CAD08196.1; PID:916502245; GSPPDB:GN00176 C;Genetics: A;Gene: ompA C;Superfamily: outer membrane protein A C;Keywords: transmembrane protein F;1-21/Domain: signal sequence #status predicted <SIG> F;22-351/Domain: outer membrane protein A #status predicted <INT> F;22-201/Domain: intramembrane #status predicted <PER> Query Match Score 7.0%; Score 24; DB 1; Length 351; Best Local Similarity 100.0%; Pred. No. 3.8e-16; Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Query Match Score 6.4%; Score 22; DB 2; Length 350; Best Local Similarity 100.0%; Pred. No. 4.2e-14; Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Qy 292 KISARGMGESENPTGTCDNVK 313 Db 298 KISARGMGESENPTGTCDNVK 319
RESULT 14		MMEBAD outer membrane protein A precursor - <i>Salmonella typhimurium</i> N;Alternate names: outer membrane major heat-modifiable protein; outer membrane protease C;Species: <i>Salmonella typhimurium</i> C;Accession: A03436; R: Fraudl, R.; Cole, S.T. Eur. J. Biochem. 134, 497-502, 1983 A;Title: Cloning and molecular characterization of the <i>ompA</i> gene from <i>Salmonella typhimurium</i> A;Reference number: A03436; MUID:93287368; PMID:6349993 A;Accession: A03436 A;Molecule type: DNA A;Residues: 1-350 <PRE> A;Cross-references: GB:X02006; PIDN:947798; PIDN:CAA26037.1; PID:9758341 C;Genetics: A;Gene: ompA A;Map position: 20 min C;Function: A;Description: required for the action of colicins and for the stabilization of matin A;Note: cannot serve as the receptor for the <i>ompA</i> -specific phages K3 and TuII C;Superfamily: outer membrane protein A C;Keywords: transmembrane protein F;1-21/Domain: signal sequence #status predicted <SIG> F;22-350/Domain: outer membrane protein A #status predicted <MAT> F;22-200/Domain: intramembrane #status predicted <INT> F;200-212/Region: alanine/proline-rich F;213-350/Domain: periplasmic #status predicted <PER> Query Match Score 6.4%; Score 22; DB 1; Length 350; Best Local Similarity 100.0%; Pred. No. 4.2e-14; Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Query Match Score 6.4%; Score 22; DB 1; Length 350; Best Local Similarity 100.0%; Pred. No. 4.2e-14; Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Qy 292 KISARGMGESENPTGTCDNVK 313 Db 298 KISARGMGESENPTGTCDNVK 319
RESULT 15		A10626 outer membrane protein A [imported] - <i>Salmonella enterica</i> subsp. <i>enterica</i> serovar Typhi C;Species: <i>Salmonella enterica</i> subsp. <i>enterica</i> serovar Typhi A;Note: this species has also been called <i>Salmonella typhi</i> C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 01-Mar-2002 C;Accession: AI0626 R;Parkhill, J.; Dougan, G.; James, K.D.; Pickard, D.; Wain, J.; Church, T.; Connor, P.; Croplin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Parr, S.; Moule, S.; O'Gaora, P. Nature 413, 848-852, 2001 A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, A;Title: Complete genome sequence of a multiple drug resistant <i>Salmonella enterica</i> serovar Typhi C;Accession: AB05026 A;Accession: AI0626 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-350 <PAR> A;Cross-references: GB:AL513382; PIDN:CAD08196.1; PID:916502245; GSPPDB:GN00176 C;Genetics: A;Gene: STY1091 C;Superfamily: outer membrane protein A C;Keywords: transmembrane protein F;1-21/Domain: signal sequence #status predicted <SIG> F;22-351/Domain: outer membrane protein A #status predicted <INT> F;22-201/Domain: intramembrane #status predicted <PER> Query Match Score 6.4%; Score 22; DB 2; Length 350; Best Local Similarity 100.0%; Pred. No. 4.2e-14; Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Query Match Score 6.4%; Score 22; DB 2; Length 350; Best Local Similarity 100.0%; Pred. No. 4.2e-14; Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Qy 292 KISARGMGESENPTGTCDNVK 313 Db 298 KISARGMGESENPTGTCDNVK 319

Tue Apr 15 09:25:25 2003

us-09-831-061-2.oligo.rpr

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Search completed: April 15, 2003, 08:56:51
Job time : 53 secs

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw mode1

Run on: April 15, 2003, 08:49:29 ; Search time 14 Seconds

(without alignments)
 1019-133 Million cell updates/secTitle: US-09-831-061-2
 Perfect score: 344
 Sequence: 1 MKAIFYLNAAPKDNTWYAGG DRRVELEVKGYKEVVTQPG 344

Scoring table: OLIGO

Gapext 60.0 , Gapext 60.0

Searched: 112892 seqs, 41476328 residues

Word size : 5
 Total number of hits satisfying chosen parameters: 8372

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries
 Database : Swissprot_40 : *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	342	99.4	344	1	OPMA_KLEEN	P24017 kibbleslella
2	53	15.4	350	1	OPMA_ENTAE	P09146 enterobacte
3	43	12.5	238	1	OPMA_CITOPR	P24016 citroba
4	33	9.6	346	1	OPMA_ECOLI	P02934 escherichia
5	29	8.4	243	1	OPMA_ESCBL	P24754 escherichia
6	27	7.8	243	1	OPMA_ESCCE	P24747 escherichia
7	24	7.0	351	1	OPMA_SHIDY	P02935 shigella dy
8	22	6.4	350	1	OPMA_SALTY	P02936 salmonella
9	20	5.8	241	1	OPMA_ESCBL	P09124 escherichia
10	19	5.5	359	1	OPMA_SERMA	P04845 serratia ma
11	17	4.9	243	1	OPMA_SEROD	P24755 serratia od
12	12	3.5	349	1	OPMA_BUGAI	P57414 buchnera ap
13	10	2.9	353	1	OPM2_HAELIN	P18368 haemophilus
14	10	2.9	359	1	OPM3_HAELIN	P45996 haemophilus
15	9	2.6	186	1	MLE1_MUGCA	P82159 mugil capit
16	9	2.6	192	1	MLEF_RAT	P17209 rattus norv
17	9	2.6	196	1	MLEF_HUMAN	P12829 homo sapien
18	9	2.6	383	1	NRL1_RHORH	P02068 rhodococcus
19	9	2.6	458	1	ARLY_VIBCH	Q9knt9 vibrio chol
20	9	2.6	1061	1	RNE_ECOLI	P21513 escherichia
21	9	2.6	1576	1	YLR3_CABEL	P41951 caenorhabdi
22	9	2.6	3866	1	HRX_MOUSE	P55200 mus musculu
23	8	2.3	28	1	OPMA_YERPS	P38399 gallus gall
24	8	2.3	51	1	LG2_TEETH	P12072 terrahymena
25	8	2.3	94	1	YBHJ_ECOLI	P75808 escherichia
26	8	2.3	1061	1	MLE1_MOUSE	P05977 mus musculu
27	8	2.3	187	1	MLE1_RAT	P02600 rattus norv
28	8	2.3	188	1	MLE1_CHICK	P02604 gallus gall
29	8	2.3	190	1	MLE1_RABBIT	P02602 orctolagus
30	8	2.3	191	1	MLE1_RABBIT	P05916 homo sapien
31	8	2.3	252	1	CRBL_BOVIN	P07318 bos taurus
32	8	2.3	260	1	H11_VOLCA	Q08844 volvox car
33	8	2.3	313	1	EBAG5_STRPL	PO4007 streptomyce

34	8	2.3	35	1	CDNC_HUMAN	P49918 homo sapien
35	8	2.3	344	1	YHJ4_YEAST	P38766 sachcharomy
36	8	2.3	346	1	RX_HUMAN	Q9Y4V3 homo sapien
37	8	2.3	353	1	OM51_HAINE	P43840 haemophilus
38	8	2.3	355	1	FKBB_HUMAN	Q14318 homo sapien
39	8	2.3	355	1	FKBB_MOUSE	Q35465 mus musculu
40	8	2.3	423	1	CCGB_MOUSE	Q8VW22 mus musculu
41	8	2.3	426	1	ASDA_NEUCCR	Q9heu5 neutrosph
42	8	2.3	437	1	EPIH_XENLA	Q91375 xenopus lae
43	8	2.3	439	1	XP2_XENLA	P17437 xenopus lae
44	8	2.3	498	1	DGT1_MOUSE	Q922A7 mus musculu
45	8	2.3	498	1	DGT1_RAT	Q98506 ratus norv
46	8	2.3	524	1	P60_LISWE	Q911W9 mus musculu
47	8	2.3	547	1	SPAK_HUMAN	Q98919 mus musculu
48	8	2.3	551	1	TF65_HUMAN	Q99600 homo sapien
49	8	2.3	553	1	ODP2_ALCBU	Q52098 alcaligenes
50	8	2.3	676	1	ICPO_HSVBJ	Q8B506 ratat norv
51	8	2.3	676	1	ICPO_HSVBK	Q98169 mus musculu
52	8	2.3	603	1	ZXDE_HUMAN	Q08919 mus musculu
53	8	2.3	603	1	NMBL_MOUSE	Q99600 homo sapien
54	8	2.3	609	1	NMBL_HUMAN	Q99600 homo sapien
55	8	2.3	622	1	3BPL_HUMAN	Q9y313 homo sapien
56	8	2.3	642	1	MB11_ARATH	Q9sav1 arabidopsis
57	8	2.3	642	1	MB11_ARATH	Q9sav1 arabidopsis
58	8	2.3	676	1	ICPO_HSVBJ	Q98169 mus musculu
59	8	2.3	676	1	ICPO_HSVBK	Q98169 mus musculu
60	8	2.3	806	1	MK07_MOUSE	Q98169 mus musculu
61	8	2.3	1051	1	TFL1_MOUSE	Q94127 mus musculu
62	8	2.3	1300	1	SAL3_HUMAN	Q9bx99 homo sapien
63	8	2.3	1385	1	CITAL_MOUSE	Q9zci4 ricettis
64	8	2.3	2774	1	MAPA_RAT	Q24926 ratat norv
65	7	2.0	14	1	LPW_ECOLI	P03053 escherichia
66	7	2.0	66	1	Y7RD_STRUJ	B22401 streptomyce
67	7	2.0	96	1	SYZ0_HUMAN	P78556 homo sapien
68	7	2.0	105	1	Y756_RICPR	Q9z958 parietaria
69	7	2.0	133	1	NL21_PARUU	Q40905 parietaria
70	7	2.0	138	1	PR28_MYTU	Q4374 mycobacteri
71	7	2.0	155	1	HES_MOUSE	Q98792 mus musculu
72	7	2.0	157	1	HES_MOUSE	Q9y543 homo sapien
73	7	2.0	173	1	HES2_HUMAN	Q9y543 homo sapien
74	7	2.0	208	1	SPC3_SRPU	F16537 strongyloc
75	7	2.0	212	1	IFP2_DETRA	Q9rsn7 deinococcus
76	7	2.0	238	1	MNBA_MAIZE	P38564 zea mays (m
77	7	2.0	243	1	RS3_SYNPE6	Q24695 synchococc
78	7	2.0	247	1	FMT_VIBIAL	Q97726 vibrio algi
79	7	2.0	256	1	Y107_NVPOV	Q10346 oryza pseu
80	7	2.0	288	1	KLF6_HUMAN	Q9Y2Y9 h. krueppel-
81	7	2.0	289	1	KLF6_MOUSE	P43670 saccharomy
82	7	2.0	289	1	YFK2_YEAST	P71697 mycobacteri
83	7	2.0	310	1	PR28_MYTU	P38981 urechis cau
84	7	2.0	317	1	RSF4_URECA	Q30620 mycobacteri
85	7	2.0	325	1	MODD_MYTU	Q50906 mycobacteri
86	7	2.0	329	1	TAL_MOUSE	P17542 homo sapien
87	7	2.0	331	1	TAL_HUMAN	Q13351 homo sapien
88	7	2.0	337	1	NCA3_YEAST	P71697 mycobacteri
89	7	2.0	345	1	CEBB_HUMAN	P17676 homo sapien
90	7	2.0	349	1	SCA3_MOUSE	Q35609 mus musculu
91	7	2.0	349	1	SCA3_MOUSE	Q35609 mus musculu
92	7	2.0	351	1	VP39_NVPOV	P17500 oryza pseu
93	7	2.0	354	1	PROW_SALTY	P17327 salmonella
94	7	2.0	362	1	KLF1_HUMAN	P17327 salmonella
95	7	2.0	370	1	KIT_FSHZ	P57939 pasteurella
96	7	2.0	379	1	AMPL_SCHEPO	Q8Z888 yersinia pe
97	7	2.0	416	1	MTP1_SYTA	P033481 psychrobact
98	7	2.0	457	1	ARLY_ECOLI	Q8Z330 escherichia
99	7	2.0	457	1	ARLY_ECOLI	Q8Z330 escherichia
100	7	2.0	457	1	ARLY_PASMU	P11447 escherichia
101	7	2.0	457	1	ARLY_YERPE	P11447 escherichia
102	7	2.0	457	1	V51K_ACUSA	P5492 apple chlor
103	7	2.0	458	1	ARLY_SALT1	Q8Z11 salmonella
104	7	2.0	458	1	ARLY_SALT1	Q8Z11 salmonella
105	7	2.0	473	1	B1AR_CANFA	P79148 canis famili
106	7	2.0	474	1	CBF5_SCHEPO	Q14007 schizosacch

		P28615	alcaligenes
107	1	R554_ALCEU	
108	1	EFD2_HUMAN	homo sapien
109	1	ROCA_BACSU	bacillus su
110	1	P54_ENTFC	enterococcus
111	1	P60_LISSE	
112	1	P60_LISIV	
113	1	HSF8_LYCPE	
114	1	CBX4_MOUSE	mus musculus
115	1	SYN2_HUMAN	homo sapien
116	1	SPH2_MOUSE	mus musculus
117	1	PAN2_HUMAN	homo sapien
118	1	FAF1_RAT	caenorhabditis elegans
119	1	E2BE_HUMAN	rattus norvegicus
120	1	SFL1_YEAST	saccharomyces cerevisiae
121	1	AFSK_STRCO	streptomyces
122	1	ZXDA_HUMAN	homo sapien
123	1	PAT3_CAEEL	caenorhabditis elegans
124	1	MKO1_HUMAN	homo sapien
125	1	GCL2_MOUSE	mus musculus
126	1	GCL2_HUMAN	homo sapien
127	1	IF2_CHLTR	chlamydia trachomatis
128	1	IF2_MOUSE	mus musculus
129	1	GND5_HUMAN	homo sapien
130	1	DC12_DRONE	homo sapien
131	1	KIT_CHICK	galus gallus
132	1	KEN5_HUMAN	homo sapien
133	1	KIT_CANFA	canis familiaris
134	1	KIT_MOUSE	mus musculus
135	1	KIT_HUMAN	homo sapien
136	1	KEMS_MOUSE	mus musculus
137	1	KIT_BOVIN	bos taurus
138	1	KFMS RAT	homo sapien
139	1	KIT_CAPII	carica papaya
140	1	KIT_FELICA	felis silvestris catus
141	1	KFMS_PELCA	chlamydia pneumoniae
142	1	TMPH_CHLTR	chlamydia trachomatis
143	1	T2D3_HUMAN	homo sapien
144	1	PIPA_DROME	drosophila melanogaster
145	1	DC11_DROME	drosophila melanogaster
146	1	MFD_BORBU	borelia burgdorferi
147	1	YAB9_YEAST	saccharomyces cerevisiae
148	1	MYSB_ACACA	acanthamoeba castellanii
149	1	V120_EBV	epstein-barr virus
150	1	MYPC_HUMAN	homo sapien
151	1	VGR3_HUMAN	homo sapien
152	1	LT23_CAEEL	caenorhabditis elegans
153	1	ICPA_HSVB	herpes simplex virus type 1
154	1	ICPA_HSVEK	herpes simplex virus type 1
155	1	DC13_DRONE	homo sapien
156	1	NEST_HUMAN	homo sapien
157	1	RRPL_PUDOM	puumala virus
158	1	CAB1_HUMAN	homo sapien
159	1	H5_COLLI	homo sapien
160	1	SASI_SPOHA	sporosarcin
161	1	ACP_MYXXA	myxococcus xanthus
162	1	N66M_ANAPL	anaplastis platys
163	1	RDGL_BOCLI	locusta migratoria
164	1	CUT0_LOCMI	archaeoglobus fulgidus
165	1	VP10_NVOP	oryzias latipes
166	1	RS6_SYN3	synchroctonellus synchroctonoides
167	1	RL7_CHLTR	chlamydia trachomatis
168	1	YL93_MYTCTU	chlamydia trachomatis
169	1	KDGL_BOCLI	locusta migratoria
170	1	CUT1_HUMAN	homo sapien
171	1	CU24_ARADI	caulobacter aculeatus
172	1	RL7_CHLTR	chlamydia trachomatis
173	1	YL93_MYTCTU	chlamydia trachomatis
174	1	YL22_ARCFU	archaeoglobus
175	1	RS12_HORVU	hordarvula vulgaris
176	1	YC15_CAUCR	caulobacter aculeatus
177	1	YGG9_YEAST	saccharomyces cerevisiae
178	1	CU19_LOCMI	locusta migratoria
179	1	CU57_ARADI	caulobacter aculeatus

253	1	PYRK__THEAC CBYC__ALCEU	Q9h136 thermoplasm	P32036 CUSCUTE ref
254	1	IF34 CAEFL	P40119 alcaligenes	098756 magnolia py
255	1	E2AA_ECOLI	Q19706 caenorhabdi	PO4938 medicago sa
256	1	XPSN_XANCP	P13810 escherichia	P12094 oryza sativ
257	1	PDUF_SALTY	P2040 xanthomonas	P04848 nicotiana t
258	1	RL7A_CHICK	P37451 salmonella	P13910 vicaria faba
259	1	RL7A_HUMAN	P34529 gallus galli	P33282 vigna ungu
260	1	NADC_METHP	P11549 homo sapien	P51106 hordeum vul
261	1	POLG_BYW	P17765 homo sapien	P90593 trypanosoma
262	1	ALP1_BACSU	P12970 mus musculus	P90778 pseudomonas
263	1	PYRF_HALN1	Q9P9m3 halobacteri	P57127 buchnera ap
264	1	YCT71_HAEIN	P44150 haemophilus	Q26756 trypanosoma
265	1	PURO_ARCPH	O20008 archaeoglob	PHBC_GHRVI
266	1	TCPN_VIBCH	P29492 vibrio chol	P45376 t poly beta
267	1	HIS1_MYCLE	P2860 methanobacte	P30692 neisseria s
268	1	FRAS1_ANSP	P17765 bean Yellow	P47669 trypanosoma
269	1	PORT_RHOB1	P13243 bacillus su	P47712 streptomyce
270	1	LAFT_VIBEA	Q03477 vibrio para	PGL1_SCLSC
271	1	CH36_DROME	P07182 drosophila	Q12708 archaeoglob
272	1	ALF_BACSP	P94453 bacillus st	Q48919 mycobacteri
273	1	FNUD_PFEAE	Q49776 mycobacteri	P30738 escherichia
274	1	PORT_RHOB1	P46107 anaerena sp	P477308 pseudomonas
275	1	BLC6_SALTY	P39767 rhodopseudo	P477312 streptomyce
276	1	LAFT_VIBEA	P13243 bacillus su	P57127 trypanosoma
277	1	CH16_DROVI	Q03477 vibrio para	P57127 trypanosoma
278	1	ER25_HUMAN	P17711 drosophila	Q12708 archaeoglob
279	1	GPD1_CANE	Q15800 homo sapien	Q48919 mycobacteri
280	1	NUPD_PFEAE	Q9P999 campylobacte	P05138 FTSZ_ECOLI
281	1	BIR7_HUMAN	P45682 pseudomonas	P477345 bacillus su
282	1	KHSE_SULTO	Q96ca5 homo sapien	P05139 heparitis b
283	1	MAIM_ECOLI	P07507 sulfobulus	P05140 heparitis b
284	1	YDJ2_SYNTP7	P03841 escherichia	P05141 heparitis b
285	1	YHCC_ECOLI	Q33701 synochococc	P05142 heparitis b
286	1	MRAW_BACSU	P45176 escherichia	P05143 hepatitis b
287	1	YCXG_BACSU	P07816 bacillus su	P05144 hepatitis b
288	1	TN11_MOUSE	Q08794 bacillus su	P05145 hepatitis b
289	1	RNHL_NEURC	Q35235 m tumor nec	P05146 hepatitis b
290	1	TDH_STRPY	Q0px88 neurospora	P05147 hepatitis b
291	1	UNRD_SYNPV	Q9ee2 r tumor nec	P05148 hepatitis b
292	1	YB98_MICPN	Q87399 synechococc	P05149 hepatitis b
293	1	MIAA_RALSO	Q50930 mycoplasma	P05150 hepatitis b
294	1	TRA0_MYCSM	Q8xb0 ralstonia s	P05151 hepatitis b
295	1	LDH_STRPY	P35983 mycobacteri	P05152 hepatitis b
296	1	PORF_TSEFL	Q99n85 streptococc	P05153 hepatitis b
297	1	KDGT_ECOLI	P07726 pseudomonas	P05154 hepatitis b
298	1	HEM2_CHLVI	Q8x497 escherichia	P05155 hepatitis b
299	1	GPDA_RHIME	P32172 escherichia	P05156 hepatitis b
300	1	G3PA_PSELE	Q59344 chlorobiun	P05157 hepatitis b
301	1	LDH_ALCEU	Q9rl16 rhizobium m	P05158 hepatitis b
302	1	G3P_2YMMO	Q59680 pseudomonas	P05159 hepatitis b
303	1	SII4_MOUSE	Q9ux7 zymomonas m	P05160 hepatitis b
304	1	SII4A_MOUSE	P09116 zymomonas m	P05161 hepatitis b
305	1	PSMC_BUCA1	P54751 m cmp-n-ace	P05162 hepatitis b
306	1	G3P_MASBA	P17541 bacterioph	P05163 hepatitis b
307	1	RTCA_HUMAN	P39013 mastigamoeb	P05164 hepatitis b
308	1	SI4A_HUMAN	Q9ne8 halobacteri	P05165 hepatitis b
309	1	I14A_PIG	P091201 h cmp-n-ace	P05166 hepatitis b
310	1	VCAA_BPT7	Q02745 s cmp-n-ace	P05167 hepatitis b
311	1	JUND_HUMAN	P197226 bacterioph	P05168 hepatitis b
312	1	END_YEASTT	P17543 homo sapien	P05169 hepatitis b
313	1	LDH_ALCEU	P39013 saccharomy	P05170 hepatitis b
314	1	DKK3_HUMAN	Q07251 alcaligenes	P05171 hepatitis b
315	1	PSBA_CHLRE	Q9ubp4 homo sapien	P05172 hepatitis b
316	1	PSBA_PEA	P07753 chlamydmon	P05173 hepatitis b
317	1	PSBA_PETHY	P06585 pisum sativ	P05174 hepatitis b
318	1	PSBA_POPDE	P04999 petunia hy	P05175 hepatitis b
319	1	PSBA_SINAL	P36491 populus del	P05176 hepatitis b
320	1	PSBA_SOYBN	P11848 sinapis alb	P05177 hepatitis b
321	1	PSBA_SPIOG	P02957 glycine max	P05178 hepatitis b
322	1	PSBA_SPITOL	P27201 spirula o	P05179 hepatitis b
323	1	PSBA_AMAHY	P02955 spinacia ol	P05180 hepatitis b
324	1	PSBA_ARATH	P02956 amaranthus	P05181 hepatitis b
325	1	PSBA_BRANA	Q33592 arabidopsis	P05182 hepatitis b
326	1	PSBA_CHIMO	P18290 brassica na	P05183 hepatitis b
327	1	COT2_BOVIN	P09752 chlamydmon	P05184 hepatitis b
328	1	COT2_CHICK	Q90733 gallus galli	P05185 hepatitis b
329	1	SV44_BRARE	Q15569 homo sapien	P05186 hepatitis b
330	1	SV44_BRARE	Q06725 brachydanio	P05187 hepatitis b
331	1	FOTSZ_ENTFA	Q88439 enterococcu	P05188 hepatitis b
332	1	Q9ctr7_bos_tauri	Q9ctr7 bos tauri	P05189 hepatitis b

399	400	1	COT2_HUMAN	P24468	homo sapien	062839	sus scrofa	062839
400	414	1	COT2_MOUSE	P43133	mus musculu	009018	rattus norv.	081928
401	6	1.7	COT2_RAT	Q92943	bos taurus	00432	cicer ariet.	TCM_CIGAR
402	6	1.7	CPT2_SOLTU	Q94mp7	helicobacte	P29463	iroshophila	CATA_BOVIN
403	6	1.7	GLYA_HELPJ	P81295	drosophil	Q92943	iroshophila	P17336
404	6	1.7	GLYA_HELPY	P81295	drosophil	P56089	mus musculu	P81067
405	6	1.7	G64C_DROME	Q9rzw8	caenorhabdi	P81295	homo sapien	Q02078
406	6	1.7	O63A_DROME	PGK8_TRYBB	caenorhabdi	P81295	canis lupus	P34649
407	6	1.7	PGKE_TRYBB	P03660	bos taurus	Q9rzw8	canis lupus	P53619
408	6	1.7	PROA_NEINB	Q919k8	trypansoma	Q919k8	canis lupus	P48444
409	6	1.7	PROA_NEINB	Q919k8	neisseria m	Q919k8	canis lupus	09zq70
410	6	1.7	PSDB_HUMAN	Q919k8	neisseria m	Q919k8	canis lupus	09zq70
411	6	1.7	COT1_RAT	Q8zhw5	rattus norv.	Q8zhw5	canis lupus	097492
412	6	1.7	COT1_BOVIN	P45069	homo sapien	P045069	canis lupus	094333
413	6	1.7	LMP2_CHICK	P0377	trypansoma	P0377	canis lupus	094333
414	6	1.7	VC2_BPLIKE	P03660	bacterioph	P03660	canis lupus	094333
415	6	1.7	COT1_MOUSE	Q00632	mus musculu	Q00632	bacterioph	094333
416	6	1.7	PSDB_HUMAN	Q00231	homo sapien	Q00231	bacterioph	094333
417	6	1.7	COT1_HUMAN	Q1589	homo sapien	P10589	bacterioph	094333
418	6	1.7	COT1_BOVIN	Q9ttr9	bos taurus	Q9ttr9	bacterioph	094333
419	6	1.7	LMP2_CHICK	Q90617	gallus galli	Q90617	bacterioph	094333
420	6	1.7	YEF5_MCTU	Q8581	mycobacteri	P04581	bacterioph	094333
421	6	1.7	FAB2_MOUSE	Q64733	mycobacteri	Q64733	bacterioph	094333
422	6	1.7	NPX1_HUMAN	Q15818	mycobacteri	Q15818	bacterioph	094333
423	6	1.7	FTS2_ARATH	Q4545	arabidopsis	Q4545	bacterioph	094333
424	6	1.7	HISX_ECOLI	P06988	escherichia	P06988	bacterioph	094333
425	6	1.7	HEN1_PASMO	B9525	pasteurella	B9525	bacterioph	094333
426	6	1.7	YAPT_ECOLI	P45546	escherichia	P45546	bacterioph	094333
427	6	1.7	EPIA_SOISO	P35021	Escherichia	P35021	bacterioph	094333
428	6	1.7	EF1G_XENLA	Q926642	Escherichia	Q926642	bacterioph	094333
429	6	1.7	NRTA_SYNP7	Q926642	Escherichia	Q926642	bacterioph	094333
430	6	1.7	NY5R_PIG	P38043	Escherichia	P38043	bacterioph	094333
431	6	1.7	SECY_METV4	Q97969	homo sapien	Q97969	bacterioph	094333
432	6	1.7	YAPT_ECOLI	P22641	methanococc	P22641	bacterioph	094333
433	6	1.7	EPIA_SOISO	P26205	methanococc	P26205	bacterioph	094333
434	6	1.7	EF1G_XENLA	P07378	methanococc	P07378	bacterioph	094333
435	6	1.7	NRTA_SYNP7	Q926642	methanococc	Q926642	bacterioph	094333
436	6	1.7	NY5R_PIG	P38043	methanococc	P38043	bacterioph	094333
437	6	1.7	FIBP_ADEP3	Q97969	methanococc	Q97969	bacterioph	094333
438	6	1.7	HSLU_AQUAE	P02457	methanococc	P02457	bacterioph	094333
439	6	1.7	YAPT_ECOLI	P22641	methanococc	P22641	bacterioph	094333
440	6	1.7	EPIA_SOISO	P07378	methanococc	P07378	bacterioph	094333
441	6	1.7	IMDH_PNECA	Q926642	methanococc	Q926642	bacterioph	094333
442	6	1.7	SECY_METTTH	P21637	pseudomonas	P21637	bacterioph	094333
443	6	1.7	COBG_PSEDE	P55055	pseudomonas	P55055	bacterioph	094333
444	6	1.7	NRH2_HUMAN	P18825	homo sapien	P18825	bacterioph	094333
445	6	1.7	A2AC_HUMAN	Q9nax8	homo sapien	Q9nax8	bacterioph	094333
446	6	1.7	AEP_YARLI	Q93442	homo sapien	Q93442	bacterioph	094333
447	6	1.7	IMDH_PNECA	Q12658	homo sapien	Q12658	bacterioph	094333
448	6	1.7	SECY_METTTH	Q26134	homo sapien	Q26134	bacterioph	094333
449	6	1.7	COBG_PSEDE	Q21637	homo sapien	Q21637	bacterioph	094333
450	6	1.7	NRH2_HUMAN	P55055	homo sapien	P55055	bacterioph	094333
451	6	1.7	AEP_YARLI	P02457	homo sapien	P02457	bacterioph	094333
452	6	1.7	IMDH_PNECA	P22641	homo sapien	P22641	bacterioph	094333
453	6	1.7	SECY_METTTH	P07378	homo sapien	P07378	bacterioph	094333
454	6	1.7	COBG_PSEDE	P21637	homo sapien	P21637	bacterioph	094333
455	6	1.7	NRH2_HUMAN	P55055	homo sapien	P55055	bacterioph	094333
456	6	1.7	A2AC_HUMAN	P02457	homo sapien	P02457	bacterioph	094333
457	6	1.7	VTNCA_NTAE	P06414	homo sapien	P06414	bacterioph	094333
458	6	1.7	ENGA_MYTCTU	P06414	homo sapien	P06414	bacterioph	094333
459	6	1.7	GAAS_CHLRE	P06414	homo sapien	P06414	bacterioph	094333
460	6	1.7	GAAS_RAT	P06414	homo sapien	P06414	bacterioph	094333
461	6	1.7	VL2_RHPV1	P22165	homo sapien	P22165	bacterioph	094333
462	6	1.7	DGT1_HUMAN	P06414	homo sapien	P06414	bacterioph	094333
463	6	1.7	PCOL_MOUSE	P06414	homo sapien	P06414	bacterioph	094333
464	6	1.7	SOX8_CHICK	P06414	homo sapien	P06414	bacterioph	094333
465	6	1.7	YUB7_MYTCTU	P06414	homo sapien	P06414	bacterioph	094333
466	6	1.7	PSBC_MARPO	P06414	homo sapien	P06414	bacterioph	094333
467	6	1.7	SYC_RHILLO	P06414	homo sapien	P06414	bacterioph	094333
468	6	1.7	GSR2_HUMAN	P06414	homo sapien	P06414	bacterioph	094333
469	6	1.7	MM11_HUMAN	P06414	homo sapien	P06414	bacterioph	094333
470	6	1.7	MOT3 YEAST	P06414	homo sapien	P06414	bacterioph	094333
471	6	1.7	DGT1_CERAE	P06414	homo sapien	P06414	bacterioph	094333
472	6	1.7	YOHG_ECOLI	P06414	homo sapien	P06414	bacterioph	094333
473	6	1.7	NASF_BACSU	P06414	homo sapien	P06414	bacterioph	094333
474	6	1.7	TRX5 MOUSE	P06414	homo sapien	P06414	bacterioph	094333
475	6	1.7	WIF1_HUMAN	P06414	homo sapien	P06414	bacterioph	094333
476	6	1.7	YAO1_SCHEO	P06414	homo sapien	P06414	bacterioph	094333
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527	6	1.7	YAO1_SCHEO	P06414	homo sapien	P06414	bacterioph	094333
528	6	1.7	YAO1_SCHEO	P06414	homo sapien	P06414		

691	1	GLT1_YEAST	Q12680	saccharomyces	0.97	1	H14_RABBIT	P02252	oryctolagus
692	1	CU05_HUMAN	Q9Y355	homo sapien	0.97	1	RPOZ_HELPY	Q21467	helicobacte
693	6	CU05_HUMAN	2298	homo sapien	1.7	1	C0XH_HUMAN	P03669	homo sapien
694	6	POLG_FMDDA	2332	f genome po	1.7	1	HMSA_SALSA	P06336	salmar salar
695	6	POLG_FMDDV	2333	f genome po	1.7	1	HOLI_BPRIT	Q38134	bacteriophila
696	6	POLG_FMDDV1	2334	f genome po	1.7	1	RS21_BRUME	Q87445	brucella me
697	6	FAS_HUMAN	2504	homo sapien	1.7	1	Y26_L_BACILLUS	Q98452	bacillus ha
698	6	FAS_RAT	2505	rattus norv	1.7	1	P49270_APTERICUS	P49270	apteticus
699	6	THYG_MOUSE	2766	thymus human	1.7	1	TXP6_APTECH	P19848	coprinus co
700	6	THYG_RAT	2768	thymus rat	1.7	1	UBIO_COPCO	P05132	ubiq
701	6	CAIC_HUMAN	3063	homo sapien	1.7	1	UBIQ_SOYBN	P05133	glycine max
702	6	POLG_PEMVC	3068	f genome po	1.7	1	P25248	human herpe	
703	6	CAIC_MOUSE	3119	caicus mouse	1.7	1	YB03_ARCEU	Q29163	archaeoglob
704	6	POLG_PSBMV	3206	f genome po	1.7	1	GEPB_BACSU	P06720	bacillus su
705	6	ERY2_SACMER	3567	erythromycin	1.7	1	RL2_ECOLI	P02428	escherichia
706	6	SPCR_HUMAN	3674	homo sapien	1.7	1	RL28_SALTY	P09943	gallus gallus
707	6	PKSM_BACSU	4273	homo sapien	1.7	1	YGRC_BACPI	P29827	streptovort
708	6	DYHA_CHLRE	4499	dyha chlre	1.7	1	CINH_STRGY	P09948	pseudomonas
709	6	HTS1_COCCA	5217	hts1 cocca	1.7	1	YR28_PSEAE	Q9htn8	chloroflexu
710	5	UHA1_CANPA	5119	uha1 canpa	1.5	1	CSNA_CHLAU	P09928	chitinase
711	5	UN46_CLOPA	514	un46 clopa	1.5	1	NSGX_HUMAN	P09924	homo sapien
712	5	LEC2_PSOISC	514	lec2 psoisc	1.5	1	Q9h64_HUMAN	P09924	homo sapien
713	5	PLAS_MICAE	515	plas micae	1.5	1	Q9h64_HUMAN	P09924	homo sapien
714	5	CD4_SHEEP	515	cd4 sheep	1.5	1	Q9h64_HUMAN	P09924	homo sapien
715	5	ANFC_CHICK	520	anfc chick	1.5	1	Q9h64_HUMAN	P09924	homo sapien
716	5	AU42_LTTR	523	au42 lttr	1.5	1	Q9h64_HUMAN	P09924	homo sapien
717	5	ANF_ANGJA	527	anf angja	1.5	1	Q9h64_HUMAN	P09924	homo sapien
718	5	IPPD_MOUSE	527	ippd mouse	1.5	1	Q9h64_HUMAN	P09924	homo sapien
719	5	PA2C_PSEPO	528	pa2c psepo	1.5	1	Q9h64_HUMAN	P09924	homo sapien
720	5	UP61_UPEIN	530	up61 upein	1.5	1	Q9h64_HUMAN	P09924	homo sapien
721	5	P2037_UPEROLEIA	530	p2037 uperoleia	1	1	Q9h64_HUMAN	P09924	homo sapien
722	5	UP62_UPEIN	535	up62 upein	1.5	1	Q9h64_HUMAN	P09924	homo sapien
723	5	VORB_METTM	535	vorb mettm	1.5	1	Q9h64_HUMAN	P09924	homo sapien
724	5	ANEV_ANGGA	536	anev angga	1.5	1	Q9h64_HUMAN	P09924	homo sapien
725	5	RL6_HALCUC	536	rl6 halcuc	1.5	1	Q9h64_HUMAN	P09924	homo sapien
726	5	PSAJ_EUGCR	537	psaj eugcr	1.5	1	Q9h64_HUMAN	P09924	homo sapien
727	5	RRPO_LSV	540	rrpo lsv	1.5	1	Q9h64_HUMAN	P09924	homo sapien
728	5	COAT_BPFP3	544	coat_bpfp3	1.5	1	Q9h64_HUMAN	P09924	homo sapien
729	5	PSAJ_PROMA	544	psaj proma	1.5	1	Q9h64_HUMAN	P09924	homo sapien
730	5	HEWP_HEWBR	545	hewp hewbr	1.5	1	Q9h64_HUMAN	P09924	homo sapien
731	5	CS32_KLEPN	546	cs32 klepn	1.5	1	Q9h64_HUMAN	P09924	homo sapien
732	5	RL32_HELPJ	547	rl32 helpj	1.5	1	Q9h64_HUMAN	P09924	homo sapien
733	5	PHNS_DESVH	547	phns desvh	1.5	1	Q9h64_HUMAN	P09924	homo sapien
734	5	SCX6_TITSE	556	scx6 titse	1.5	1	Q9h64_HUMAN	P09924	homo sapien
735	5	H2AQ_HUMAN	556	h2aq human	1.5	1	Q9h64_HUMAN	P09924	homo sapien
736	5	HPIS_RHOGL	557	hpis rhogl	1.5	1	Q9h64_HUMAN	P09924	homo sapien
737	5	IPL_SOIME	557	ipl soime	1.5	1	Q9h64_HUMAN	P09924	homo sapien
738	5	RUBR_TREPA	557	ruber trepa	1.5	1	Q9h64_HUMAN	P09924	homo sapien
739	5	YABQ_ECOLI	561	yabq_ecoli	1.5	1	Q9h64_HUMAN	P09924	homo sapien
740	5	QH17777_HOMO	561	qh17777 homo	1.5	1	Q9h64_HUMAN	P09924	homo sapien
741	5	DESLFIVORIB	561	desulfivorib	1.5	1	Q9h64_HUMAN	P09924	homo sapien
742	5	PHB2_SALSA	561	phb2 salsa	1.5	1	Q9h64_HUMAN	P09924	homo sapien
743	5	PPSA_ERWEHE	561	ppsa_erwehe	1.5	1	Q9h64_HUMAN	P09924	homo sapien
744	5	CXH3_NAJKA	562	cxh3 najka	1.5	1	Q9h64_HUMAN	P09924	homo sapien
745	5	ANP1_AUSBR	562	anp1_ausbr	1.5	1	Q9h64_HUMAN	P09924	homo sapien
746	5	ANP2_AUSBR	563	anp2_ausbr	1.5	1	Q9h64_HUMAN	P09924	homo sapien
747	5	YRKD_BACSU	563	yrkd_bacsu	1.5	1	Q9h64_HUMAN	P09924	homo sapien
748	5	IPR_SOIME	564	ipr soime	1.5	1	Q9h64_HUMAN	P09924	homo sapien
749	5	RUBR_LAMBBD	564	ruber lambbd	1.5	1	Q9h64_HUMAN	P09924	homo sapien
750	5	LHA3_NAJKA	565	lha3 najka	1.5	1	Q9h64_HUMAN	P09924	homo sapien
751	5	YP7A_TNVD	565	yp7a_tnvd	1.5	1	Q9h64_HUMAN	P09924	homo sapien
752	5	LHA2_RHOPA	566	lha2 rhopa	1.5	1	Q9h64_HUMAN	P09924	homo sapien
753	5	CYC3_DESAC	568	cyc3_desac	1.5	1	Q9h64_HUMAN	P09924	homo sapien
754	5	PLE2_PSEAM	568	ple2_pseam	1.5	1	Q9h64_HUMAN	P09924	homo sapien
755	5	VHTJ_LAMBD	568	vhtj_lambd	1.5	1	Q9h64_HUMAN	P09924	homo sapien
756	5	YLK5_CAEEL	568	ylk5_caeel	1.5	1	Q9h64_HUMAN	P09924	homo sapien
757	5	MOP_HAEIN	569	mop_haein	1.5	1	Q9h64_HUMAN	P09924	homo sapien
758	5	CSP1_ECOLI	570	csp1_ecoli	1.5	1	Q9h64_HUMAN	P09924	homo sapien
759	5	CSPJ_SALTI	570	cspj_salti	1.5	1	Q9h64_HUMAN	P09924	homo sapien
760	5	RS21_CAME	570	rs21_came	1.5	1	Q9h64_HUMAN	P09924	homo sapien
761	5	SAS1_BACCE	570	sas1_bacce	1.5	1	Q9h64_HUMAN	P09924	homo sapien
762	5	MBTH_MYCTU	571	mbth_myctu	1.5	1	Q9h64_HUMAN	P09924	homo sapien
763	5	V07K_PVXB	571	v07k_pvxb	1.5	1	Q9h64_HUMAN	P09924	homo sapien

837	1	KEF1_ECOLI	052281 escherichia	P01626 mus musculu
838	5	NUGG_SOYBN	P31174 glycine max	P01623 mus musculu
839	5	FIS_PASH	P04367 pasteurilla	P36496 pediococcus
840	5	MOBS_THIFE	P20086 thiobacillus	P47389 mycoplasma
841	5	RS20_CHLMU	Q9PjC chlamydia m	P21214 bovinus
842	5	VHED_PPFLH	Q07481 bacteriophaga	057114 haemophilus
843	5	NIC1_HUMAN	Q9ug19 homo sapien	P39740 bacillus su
844	5	PLAS_CUCPE	P00292 cucurbita P	P03976 mus musculu
845	5	RS20_CHLBN	Q9Z72 chlamydia p	P04537 bos taurus
846	5	Y233_MYCGE	P47475 mycoplasma	M01419 scrofa
847	5	Y837_NEIMB	Q9125 neisseria m	SSIF_BALVO
848	5	YKPB_YEAST	P36055 streptomyce	Q9r645 mycoplasma
849	5	RS14_RHIME	Q9247 rhizobium m	P43043 haemophilus
850	5	YG75_MYCPN	Q26177 mycoplasma	068475 mycobacteri
851	5	ARSC_NEIMG	P9554 neisseria g	Q10501 mycobacteri
852	5	FLAF_CAUCR	P21295 caulobacter	SFP3_BOVIN
853	5	GLRX_RICCO	P55143 ricinus com	PFLHD_PROMI
854	5	SECG_STRCO	Q9z221 streptomyce	NU3M_MYTED
855	5	TXOB_HADIN	Q9b102 hadronychae	P152650 strengolyc
856	5	Y224_METTCH	Q26126 methanobact	052666 rhizobium m
857	5	ANFB_BOVIN	P1304 bos taurus	Q91qu0 neisseria m
858	5	CHLB_NEPEX	P37950 nephrolypis	P01748 mus musculu
859	5	RL21_HAEIN	P44543 haemophilus	P28137 plethodon j
860	5	TCTA_HUMAN	P57738 homo sapien	Q00568 mytilus ediu
861	5	Y446_NEIMA	Q91j14 neisseria m.	P109_HAEIN
862	5	YF94_MYCPN	P75101 mycoplasma	P126_RHIME
863	5	YGBQ_ECOLI	Q46994 escherichia	Q99466 rhesus m
864	5	KAC6_RABTU	P03984 oryzolagrus	P07793 psammochinu
865	5	LAC2_MOUSE	P01644 mus musculus	P33577 petromyzon
866	5	LAC2_RAT	P20677 rattus norv	P25498 naja oxiana
867	5	LAC3_MOUSE	P01845 mus musculu	P20577 bacillus su
868	5	Y4EB_RHISM	P26525 rhizobium s	Q9c188 pasteurella
869	5	HXB4_BRARE	P2274 brachydanio	Q08790 pseudomonas
870	5	INS_SHEEP	P01318 ovis aries	P07938 erwilia chr
871	5	LAC1_MOUSE	P01843 mus musculus	P01627 psammochinu
872	5	LAC1_HUMAN	P01842 homo sapien	P38744 saecharomyces
873	5	LAC1_PIG	P01845 mus musculu	Q9Ab51 aeropyrum p
874	5	LAC1_RABIT	P01846 oryzolagrus	Q9PjZ0 campylobact
875	5	YOPN_BACSU	Q34369 bacillus su	P55282 drosophila
876	5	ATPR_DROME	P2407 drosophila	P30167 archaeoglob
877	5	RL12_ARCFU	P2880 archaeoglob	P03213 bacillus su
878	5	THIO_STRAU	P33191 streptomyce	P046618 bacillus su
879	5	VHSB_BPT3	P20322 bacteriophaga	P38442 aeropyrum p
880	5	YBHO_YEAST	P38186 saecharomyces	P20753 mus musculu
881	5	CYC_APIME	P00038 apis mellif	P040753 mus musculu
882	5	GRO_HUMAN	P0341 homo sapien	P040753 mus musculu
883	5	INS_PIG	P01315 sus scrofa	P040753 mus musculu
884	5	H1S2_BRUNE	P04948 schizosacch	P040753 mus musculu
885	5	T2AG_SCHPO	P05590 murine coro	P040753 mus musculu
886	5	VNS2_CVWMH	P094f3 pastuerella	P040753 mus musculu
887	5	Y668_PASNU	P00030 eisensteinii	P040753 mus musculu
888	5	Y892_EISFO	P0341 human papill	P040753 mus musculu
889	5	Y905_NPYAC	P33382 listeria mo	P040753 mus musculu
890	5	VAPI_BACNO	P4520 autoxrapha	P040753 mus musculu
891	5	Y826_RICBR	P57825 pastuerella	P040753 mus musculu
892	5	Y065_RALSO	P17577 escherichia	P040753 mus musculu
893	5	CYC_ISSOR	P08w99 ralstonia s	P040753 mus musculu
894	5	TRP5_BOVIN	P00041 issatchenki	P040753 mus musculu
895	5	Y208_LISMO	Q9nyv9 bos taurus	P040753 mus musculu
896	5	YK21_CAEBL	P34328 caenorhabdi	P040753 mus musculu
897	5	Y205_PASNU	Q8zC96 yersinia pe	P040753 mus musculu
898	5	YBAE_ECOLI	P9yw99 aeropyrum p	P040753 mus musculu
899	5	Y208_LISMO	P14626 rana catesbe	P040753 mus musculu
900	5	Y208_LISMO	P05397 synechocyst	P040753 mus musculu
901	5	YK21_YERPE	P32262 bacillus su	P040753 mus musculu
902	5	YRJ2_AEEPE	P03265 psammochinu	P040753 mus musculu
903	5	Y110_HUMAN	P14626 rana catesbe	P040753 mus musculu
904	5	Y546_SYNYY3	P03265 rhaebacter	P040753 mus musculu
905	5	YDVS_BACSU	P03262 bacillus su	P040753 mus musculu
906	5	CORD_BPFD	P03673 bacteriophaga	P16886 strengolyc
907	5	GLNB_RHIME	P04053 rhaebacter	P37156 tachygilossu
908	5	GLNB_RHOMA	P13556 rhodobacter	PCD5_HUMAN
909	5	H2R3_LITPI	P05989 lytechinus	P040753 mus musculu

983 5 1.5 125 1 RS13_SYNP6
 984 5 1.5 125 1 RS25_HUMAN
 985 5 1.5 125 1 RS25_ARCEU
 986 5 1.5 125 1 SPH1_PYRAE
 987 5 1.5 125 1 TRPR_YEPE
 988 5 1.5 125 1 YBAN_ECOLI
 989 5 1.5 125 1 YES2_YEAST
 990 5 1.5 126 1 ANFC_BOVIN
 991 5 1.5 126 1 ANFC_HUMAN
 992 5 1.5 126 1 ANFC_MOUSE
 993 5 1.5 126 1 ANFC_PIG
 994 5 1.5 126 1 ANFC_RAT
 995 5 1.5 126 1 ANFC_SHEEP
 996 5 1.5 126 1 CD59_RAT
 997 5 1.5 126 1 H2A_CABEL
 998 5 1.5 126 1 MS10_CAEEL
 999 5 1.5 126 1 MS31_CAEEL
 1000 5 1.5 126 1 MS33_CAEEL

ALIGNMENTS

RESULT 1
 OMPA_KLEPN ID OMPA_KLEPN STANDARD; PRT; 344 AA.

AC P24077; 069435; DT 01-MAR-1992 (Ref. 21, Created)
 DT 15-DEC-1998 (Ref. 37, Last sequence update)
 DE Outer membrane protein A precursor (Outer membrane protein II).

GN OMPA.
 OC Klebsiella pneumoniae.
 OC Bacteriia; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Klebsiella.
 OX NCBI_TAXID=573;

RN [1]

RP STRAIN=RV 308;

RX MEDLINE=9819544; PubMed=9524233;

RA Nguen T.N., Samuelson P., Sterky F., Merle-Poitte C., Robert A.,

RA Bausant T., Haewu J.F., Uhlen M., Binz H., Stahl S.;

RT "Chromosomal sequencing using a PCR-based biotin-Capture method

RT allowed isolation of the complete gene for the outer membrane protein

RT of Klebsiella pneumoniae." Gene 210:93-101 (1998).

RN SEQUENCE OF 93-315. FROM N.A.

RC STRAIN=LD119;

RX MEDLINE=9205252; PubMed=1955870;

RA Lawrence J.G., Ochman H., Hartl D.L.;

RA "Molecular and evolutionary relationships among enteric bacteria." ;

RL J. Gen. Microbiol. 137:1911-1921 (1991).

CC FUNCTION: REQUIRED FOR THE ACTION OF COLICINS K AND L AND FOR THE

CC STABILIZATION OF MATING AGGREGATES IN CONJUGATION. SERVES AS A

CC RECEPTOR FOR A NUMBER OF T-EVEN LIKE PHAGES. ALSO ACTS AS A'PORIN

CC SOLUTES (BY SIMILARITY). ;

CC -I- SUBUNIT: MONOMER (PROBABLE).

CC -I- SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane.

CC --I- SIMILARITY: BELONGS TO THE OMPA FAMILY.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration

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CC modified and this statement is not removed. Usage by and for commercial

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CC or send an email to license@isb-sib.ch).

DR EMBL; A000998; CA04450.1; -.

DR EMBL; M63355; AAA25119.1; -.

DR HSSP; P02934; IQUP.

DR InterPro; IPR001145; Bac_OmpA.
 DR InterPro; IPR000498; OmpA_tmem.
 DR Pfam; PF00691; OmpA; 1.
 DR PRINTS; PRO1021; OMPADOMAIN.
 DR PRODOM; PD000930; Bac_OmpA; 1.
 DR PROSITE; PS01068; OMPA; 1.
 DR Outer membrane. Transmembrane: Phage recognition; Signal; Repeat;
 KW Porin.
 FT SIGNAL 1 ? ?
 FT CHAIN 1 ? 344
 FT TRANSMEM 15 28
 FT TRANSMEM 48 60
 FT TRANSMEM 63 78
 FT TRANSMEM 90 100
 FT TRANSMEM 104 119
 FT TRANSMEM 140 151
 FT TRANSMEM 157 173
 FT TRANSMEM 179 190
 FT DOMAIN 199 206
 FT REPEAT 199 206
 FT REPEAT 201 202
 FT REPEAT 203 204
 FT REPEAT 205 206
 FT DOMAIN 255 299
 FT CONFLICT 309 321
 SQ SEQUENCE 344 AA; BY SIMILARITY.
 Query Match 99.4%; Score 342; Pred. No. 0;
 Best Local Similarity 100.0%; Mismatches 0; Indels 0; Gaps 0;
 Matches 342; Conservative 342; Sequence 344 AA; MW: AC88AAE327871B16 CRC64;

RESULT 2
 OMPA_ENTAE ID OMPA_ENTAE STANDARD; PRT; 350 AA.

AC P01464;

DT 01-MAR-1989 (Rel. 10, Created)

DT 01-MAR-1989 (Rel. 10, Last sequence update)

DE Outer membrane protein A precursor.

GN OMPA.

OS Enterobacter aerogenes (Aerobacter aerogenes),

OC Enterobacter; gamma subdivision; Enterobacteriaceae.

NCBI_TAXID=548;

RN [1]

RP SEQUENCE FROM N.A.

- [1] SEQUENCE FROM N.A.
STRAIN=K12;
RC MEDLINE=81170587; PubMed=6260961;
RX Beck E., Bremer E.;
RT "Nucleotide sequence of the gene ompA coding the outer membrane protein II of *Escherichia coli* K-12.";
RL Nucleic Acids Res. 8:3011-3024(1980).
RN [2]
SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=81170587; PubMed=6260961;
RA Movva N.R., Nakamura K., Inouye M.;
RT "Gene structure of the OmpA protein, a major surface protein of *Escherichia coli* required for cell-cell interaction.";
J. Mol. Biol. 143:317-328(1980).
RN [3]
SEQUENCE FROM N.A.
RP STRAIN=K12 / MG165;
RX MEDLINE=974126617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vives J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J.J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
RT "The complete genome sequence of *Escherichia coli* K-12.";
Science 277:1453-1474(1997).
RN [4]
SEQUENCE FROM N.A.
RP STRAIN=K12;
RX MEDLINE=97061202; PubMed=8905232;
RA Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,
RA Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
RA Kimura S., Kitagawa M., Makino K., Masuda S., Mikl T., Mizobuchi K.,
RA Mori H., Motomura K., Nakamura Y., Nishio Y., Saito N.,
RA Sampai G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
RA Yano M., Horiuchi T.;
RT "A 718-kb DNA sequence of the *Escherichia coli* K-12 genome
corresponding to the 12.7-28.0 min region on the linkage map.";
DNA Res. 3:137-155(1996).
RN [5]
SEQUENCE FROM N.A.
RP STRAIN=K12;
RX MEDLINE=0157:H7 / EDL033 / ATCC 700927;
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Postal G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grotbeck E.J., Davis N.W., Lim A., Dimmler E.T., Potamitis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RT "Genome sequence of enterohaemorrhagic *Escherichia coli* O157:H7;"
Nature 409:529-533(2001).
RN [6]
SEQUENCE FROM N.A.
RP STRAIN=K12;
RX MEDLINE=21156231; PubMed=11228796;
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA Iida T., Takami H., Honda T., Sasaki K., Ogawara N., Yasunaga T.,
RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;
RT "Complete genome sequence of enterohaemorrhagic *Escherichia coli*
O157:H7 and genomic comparison with a laboratory strain K-12.";
DNA Res. 8:11-22(2001).
RN [7]
SEQUENCE OF 22-346.
RC STRAIN=K12;
RX MEDLINE=81054820; PubMed=7001461;
RA Chen R., Schmidmayer W., Kramer C., Chen-Schmeisser U., Henning U.;
RT "Primary structure of major outer membrane protein II (ompA protein)
of *Escherichia coli* K-12.";
RL Proc. Natl. Acad. Sci. U.S.A. 77:4592-4596(1980).
RN [8]
SEQUENCE OF 22-32.
RC STRAIN=K12 / W3110;
- Pasquali C., Sanchez J.-C., Ravier F., Golaz O., Appel R.D., Bairach A., Frutiger S., Paquet N., Wilkins M., Appel R.D., Bairach A., Hochstrasser D.F.;
RA Submitted (SP-1994) to the SWISS-PROT data bank.
RN [9]
SEQUENCE OF 22-34.
RC STRAIN=K12 / EMG2;
RX MEDLINE=97443955; PubMed=9298646;
RA Link A.J., Robison K., Church G.M.;
RT "Comparing the predicted and observed properties of proteins encoded in the genome of *Escherichia coli* K-12.";
RL Electrophoresis 18:1259-1313(1997).
RN [10]
SEQUENCE OF 22-26.
RC STRAIN=K12 / K3110;
RX MEDLINE=98291816; PubMed=9629924;
RA Molloy M.P., Herbert B.R., Walsh B.J., Tyler M.I., Traini M.,
RT "Extraction of membrane proteins by differential solubilization for separation using two-dimensional gel electrophoresis.";
Electrophoresis 19:837-844(1998).
RN [11]
SEQUENCE OF 22-26.
RC STRAIN=K12 / K3110;
RX MEDLINE=98291816; PubMed=9629924;
RA Sanchez J.-C., Hochstrasser D.F., Williams K.L., Gooley A.A.;
RT "Mutants resistant to phage entry.";
J. Bacteriol. 174:3036-3046; Published=3902787;
RA Morona R., Kramer C., Henning U.;
RT "Bacteriophage receptor area of outer membrane protein OmpA of *Escherichia coli* K-12.";
J. Bacteriol. 164:539-543(1985).
RN [12]
SEQUENCE OF 22-26.
RC STRAIN=K12;
RX MUTANTS RESISTANT TO PHAGE ENTRY;
RA Morona R., Kramer C., Henning U.;
RT "Pore-forming activity of OmpA protein of *Escherichia coli* K-12.";
J. Bacteriol. 174:3036-3046; Published=3902787;
RA Morona R., Kramer C., Henning U.;
RT "Bacteriophage receptor area of outer membrane protein OmpA of *Escherichia coli* K-12.";
J. Bacteriol. 164:539-543(1985).
RN [13]
SEQUENCE OF 22-26.
RC STRAIN=K12;
RX PORIN ACTIVITY;
RA Sugawara E., Nikaido H.;
RT "Pore-forming activity of OmpA protein of *Escherichia coli* K-12.";
J. Bacteriol. 174:3036-3046; Published=3902787;
RA Gromiha M.M., Ponuswamy P. K.;
RT "Prediction of transmembrane beta-strands from hydrophobic topology.";
RA Gromiha M.M., Ponuswamy P. K.;
RT "Prediction of transmembrane beta-strands from hydrophobic characteristics of proteins.";
Int. J. Pept. Protein Res. 42:420-431(1993).
RN [14]
SEQUENCE OF 22-26.
RC STRAIN=K12;
RX TOPOLOGY;
RA Koebnik R.;
RT "Structural and functional roles of the surface-exposed loops of the beta-barrel membrane protein OmpA from *Escherichia coli* K-12.";
J. Bacteriol. 181:3608-3634(1999).
RN [15]
SEQUENCE OF 22-26.
RC STRAIN=K12;
RX X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 22-192.
RA Pautsch A., Schulz G.E.;
RT "Structure of the outer membrane protein A transmembrane domain.";
J. Mol. Biol. 273:282(2000).
RN [16]
SEQUENCE OF 22-26.
RC STRAIN=K12;
RX X-RAY CRYSTALLOGRAPHY (1.15 ANGSTROMS).
RA Pautsch A., Schulz G.E.;
RT "High resolution structure of the OmpA membrane domain.";
J. Mol. Biol. 298:273-282(2000).
RN [17]
SEQUENCE OF 22-26.
RC STRAIN=K12;
RX MASS SPECTROMETRY;
RA Le Coutre J., Whitelegge J.P., Gross A., Turk E., Wright E.M.,

CC RECEPTOR FOR A NUMBER OF T-EVEN LIKE PHAGS. ALSO ACTS AS A PORIN
 CC WITH LOW PERMEABILITY THAT ALLOWS SLOW PENETRATION OF SMALL
 CC SOLUTES (BY SIMILARITY).
 CC -|- SUBUNIT: MONOMER (PROBABLE).
 CC -|- SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane.
 CC -|- MISCELLANEOUS: THE SEQUENCE SHOWN IS THAT OF STRAINS ATCC 35471
 CC AND ATCC 35472.
 CC -|- SIMILARITY: BELONGS TO THE OMPA FAMILY.

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 CC or send an email to license@isb-sib.ch).
 DR EMBL; M63352; AAA24236.1;
 DR EMBL; M63351; AAA24232.1;
 DR HSSP; P02934; IQJP.
 DR InterPro; IPR001145; Bac_OmpA.
 DR InterPro; IPR000498; OmpA_tmem.
 DR Pfam; PF00691; OmpA; 1.
 DR Pfam; PF01389; OmpA_membrane; 1.
 DR ProdDom; P0000930; Bac_OmpA; 1.
 DR PROSITE; PS01058; OMPA; 1.
 KW Outer membrane; Transmembrane; Phage recognition; Repeat; Porin.
 FT NON_TER 1
 FT TRANSMEM <1 8 POTENTIAL.
 FT TRANSMEM 12 27 POTENTIAL.
 FT TRANSMEM 48 59 POTENTIAL.
 FT TRANSMEM 65 81 POTENTIAL.
 FT TRANSMEM 87 98 POTENTIAL.
 FT DOMAIN 107 114 4 X 2 AA TANDEM REPEATS OF A-P.
 FT REPEAT 107 108 1.
 FT REPEAT 109 110 2.
 FT REPEAT 111 112 3.
 FT REPEAT 113 114 4.
 FT DOMAIN 163 207 OMPA-LIKE.
 FT DISULFID 217 229 BY SIMILARITY.
 FT VARIANT 39 39 E -> D (IN STRAIN ATCC 35469).
 FT NON_TER 243 243 MW: 26144 MW;
 SQ SEQUENCE 243 AA: TKHFTLKSVDLFENFKATLKPEQ 243

Query Match 7.8% Score 27; DB 1; Length 243;
 Best Local Similarity 100.0% Pred. No. 2.6e-20; Mismatches 0; Indels 0; Gaps 0;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 93 LTAKLGYPTDLDIYTRGGWVRAD 119
 Db 1 LTAKLGYPTDLDIYTRGGWVRAD 27

RESULT 7
 OMPA_SHIDY STANDARD PRT; 351 AA.
 AC P02935;
 ID OMPA_SHIDY STANDARD PRT; 350 AA.
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Outer membrane protein A precursor (Outer membrane protein III).
 GN OMPA.
 OS Shigella dysenteriae.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 Shigella.
 NCBI_TAXID=622;
 RN [1]
 RP SOURCE FROM N.A.
 RX MEDLINE=822141; PubMed=6283478;
 RA Braun G.; Cole S.T.;
 RT "The nucleotide sequence coding for major outer membrane protein Ompa
 of Shigella dysenteriae.";
 RN [1]

RL Nucleic Acids Res. 10:2367-2378(1982).
 CC -|- FUNCTION: REQUIRED FOR THE ACTION OF COLICINS K AND L AND FOR THE
 CC STABILIZATION OF MATING AGGREGATES IN CONJUGATION. SERVES AS A
 CC RECEPTOR FOR A NUMBER OF T-EVEN LIKE PHAGES. ALSO ACTS AS A PORIN
 CC WITH LOW PERMEABILITY THAT ALLOWS SLOW PENETRATION OF SMALL
 CC SOLUTES (BY SIMILARITY).
 CC -|- SUBUNIT: MONOMER (PROBABLE).
 CC -|- SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane.
 CC -|- SIMILARITY: BELONGS TO THE OMPA FAMILY.
 CC -|- SIMILARITY: BELONGS TO THE OMPA FAMILY.
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 CC or send an email to license@isb-sib.ch).
 DR EMBL; Y01344; CA24638.1;
 DR PIR; A03435; MMEDAD.
 DR HSSE; P02934; IQJP.
 DR InterPro; IPR001145; Bac_OmpA.
 DR InterPro; IPR000498; OmpA_tmem.
 DR Pfam; PF00691; OmpA; 1.
 DR Pfam; PF01389; OmpA_membrane; 1.
 DR PRINTS; PRO10021; OMPADOMAIN.
 DR PRODOM; PD000930; Bac_OmpA; 1.
 DR PROSITE; PS01068; OMPA; 1.
 KW Outer membrane; Transmembrane; Phage recognition; Signal; Repeat;
 KW Porin.
 FT SIGNAL 1 21
 FT CHAIN 22 351 OUTER MEMBRANE PROTEIN A.
 FT TRANSMEM 22 40 POTENTIAL.
 FT TRANSMEM 55 67 POTENTIAL.
 FT TRANSMEM 70 85 POTENTIAL.
 FT TRANSMEM 97 107 POTENTIAL.
 FT TRANSMEM 111 126 POTENTIAL.
 FT TRANSMEM 147 158 POTENTIAL.
 FT TRANSMEM 164 180 POTENTIAL.
 FT TRANSMEM 186 197 POTENTIAL.
 FT DOMAIN 206 213 4 X 2 AA TANDEM REPEATS OF A-P.
 FT REPEAT 206 207 1.
 FT REPEAT 208 209 2.
 FT REPEAT 210 211 3.
 FT REPEAT 212 213 4.
 FT DOMAIN 262 306 OMPA-LIKE.
 FT DISULFID 316 328 BY SIMILARITY.
 SQ SEQUENCE 351 AA: TKHFTLKSVDLFENFKATLKPEQ 233
 Query Match 7.0% Score 24; DB 1; Length 351;
 Best Local Similarity 100.0% Pred. No. 4.8e-17; Mismatches 0; Indels 0; Gaps 0;

QY 210 TKHFTLKSVDLFENFKATLKPEQ 233
 ID OMPA_SALTY STANDARD PRT; 350 AA.
 AC P02936;
 ID OMPA_SALTY STANDARD PRT; 350 AA.
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Outer membrane protein A precursor (Outer membrane protein 33k) (Outer
 DE membrane major heat-modifiable protein).
 GN OMPA OR STM1070.
 OS Salmonella typhimurium.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Salmonella.
 NCBI_TAXID=602;
 RN [1]

RP	SEQUENCE FROM N.A.	Qy	292 KISARGMGESNPVGTNTCDNVK
RX	MEDLINE-8327366; PubMed-6349993;	313	
RA	Freudl R., Cole S.T.;		
RT	"Cloning and molecular characterization of the <i>ompA</i> gene from		
RL	Salmonella typhimurium."		
RN	Eur. J. Biochem. 134:497-502(1983).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=LT2 / SGSC1412 / ATCC 700720;		
RX	MEDLINE-21534948; PubMed-11677609;		
RA	McClelland M., Sanderson K.E., Sleath J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K.;		
RN	"Complete genome sequence of <i>Salmonella enterica</i> serovar Typhimurium LT2."		
RN	Nature 413:852-856(2001).		
CC	-1- FUNCTION: REQUIRED FOR THE ACTION OF COLICINS K AND L AND FOR THE STABILIZATION OF MATING AGGREGATES IN CONJUGATION. SERVES AS A RECEPTOR FOR A NUMBER OF T-EVEN LIKE PHAGES. ALSO ACTS AS A POREN CC SOLUTES (BY SIMILARITY).		
CC	-1- SUBUNIT: MONOMER (PROBABLE).		
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane		
CC	-1- SIMILARITY: BELONGS TO THE OMPA FAMILY.		
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DR	EMBL; X0006; CAA6037_1; -.		
DR	EMBL; AB008746; AAL20003_1; -.		
DR	PIR; A04436; MMDBAT.		
DR	HSSP; P02934; 1QJP.		
DR	StGene; SG10263; OmpA.		
DR	InterPro; IPR001145; Bac_OmpA.		
DR	InterPro; IPR000498; OmpA_tmem.		
DR	Pfam; PF00691; OmpA_1.		
DR	Pfam; PF1388; OmpA_membrane; 1.		
DR	Prosite; PS000930; Bac_OmpA_1.		
DR	Prosite; PS01068; OMPA_1.		
KW	Outer membrane; Transmembrane; Phage recognition; Signal; Repeat; Porin; Complete proteome.		
FT	SIGNAL 1 21	OUTER MEMBRANE PROTEIN A.	
FT	CHAIN 22 350		
FT	TRANSMEM 27 40	POTENTIAL.	
FT	TRANSMEM 55 67	POTENTIAL.	
FT	TRANSMEM 70 85	POTENTIAL.	
FT	TRANSMEM 97 107	POTENTIAL.	
FT	TRANSMEM 111 126	POTENTIAL.	
FT	TRANSMEM 146 157	POTENTIAL.	
FT	TRANSMEM 163 179	POTENTIAL.	
FT	TRANSMEM 185 196	POTENTIAL.	
FT	DOMAIN 205 212	4 X 2 AA TANDEM REPEATS OF A-P.	
FT	REPEAT 205 206	1.	
FT	REPEAT 207 208	1.	
FT	REPEAT 209 210	3.	
FT	REPEAT 211 212	4.	
FT	DOMAIN 261 305	OMPA-LIKE.	
FT	DISULFID 315 327	BY SIMILARITY.	
FT	CONFFLICT 114 114	V -> F (IN REF. 1).	
FT	CONFFLICT 247 247	S -> I (IN REF. 1).	
SQ	SEQUENCE 350 AA; 37515 MW;	B4AC52C85DF54FE CRC64;	
Query Match	6.4%	Score 22; DB 1; Length 350;	
Best Local Similarity	100.0%	Pred. No. 5.9e-15;	
Matches 22;	Conservative 0;	Mismatches 0; Indels 0; Gaps 0;	
			K -> Q (IN STRAIN ATCC 29907 AND

AC P45996; 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Outer membrane Protein P5 precursor (OMP P5) (Fimbrin).
GN OMPA OR OMPPs.
OS Haemophilus influenzae.
OC Haemophilus; Proteobacteria; gamma subdivision; Pasteurellaceae;
OX NCBI_TAXID=727;
RN [1] PROTEIN DOES NOT BIND CALCIUM.
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX STRAIN-NTH1_1128;
RX MEDLINE=9422575; PubMed=7909539;
RA Sirakova T., Kolattukudy P.E., Murwin D., Billy J., Leake E.,
RA Lim D., Demaria T., Bakalcz L.;
RT "Role of fimbriae produced by non-typeable Haemophilus influenzae in
RR pathogenesis and protection against otitis media and relatedness
RT of the fimbrial subunit to outer membrane protein A.;"
RL Infect. Immun. 62:2002-2010(1994).
CC |- FUNCTION: ACTS AS A FIBRILLAE SUBUNIT.
CC |- SIMILARITY: BELONGS TO THE OMPA FAMILY.
CC -----
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CC -----
DR HSSP; AA2448; AA24959; 1; -
DR InterPro; IP02934; IBW.
DR InterPro; IP00145; Bac_OmpA.
DR PF00098; OmpA_tmem.
DR PF00691; OmpA; 1.
DR PF01389; OmpA_membrane; 1.
DR PRODOM; PRO1021; OMPADOMA1_N.
DR PRODOM; PD000930; Bac_OmpA; 1.
DR PROSITE; PS01068; OMPA; FALSE_NEG.
KW Outer membrane; Transmembrane; Porin; Signal; Fimbria.
FT SIGNAL 1 21 OUTER MEMBRANE PROTEIN_P5.
FT CHAIN 22 359 BY SIMILARITY.
FT DISULFDID 332 344 OMPA-LIKE.
FT DOMAIN 278 322 OMPA-LIKE.
SQ SEQUENCE 359 AA; 38340 MW; 576BIC59B4818C37 CRC64;

Query Match 2.9%; Score 10; DB 1; Length 359;
Best Local Similarity 100.0%; Pred. No. 0.02%;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 321 CLAPDRVEI 330
Db 344 CLAPDRRVEI 353

RESULT 15
MLE1_MUGCA STANDARD; PRT; 1.86 AA.
ID MLE1_MUGCA
AC P02159;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Myosin light chain 1, skeletal muscle isoform (Al catalytic) (Alkali)
DE (LC-1) (LC1).
OS Mugil capito (Grey mullet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterigii; Percomorpha; Mugilomorpha; Mugilidae;
OC Liza
OX NCB_TaxID=30804;

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: April 15, 2003, 08:51:59 ; Search time 34 Seconds

(without alignments)
2084.712 Million cell updates/sec
1 MKAIFVNAAPKDNTWAGG.....DRVEEVKGYKEVVTQPAG 344

Title: US-09-831-061-2

Perfect score: 344

Sequence: 1 MKAIFVNAAPKDNTWAGG.....DRVEEVKGYKEVVTQPAG 344

Scoring table: OLIGO

Gapext 60.0 , Gapext 60.0

Searched: 671580 seqs, 206047115 residues

Word size : 5

Total number of hits satisfying chosen parameters: 39383

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : SPTREMBL_21_*

- 1: sp_bacteria:*
- 2: sp_fungi:*
- 3: sp_invertebrate:*
- 4: sp_human:*
- 5: sp_mammal:*
- 6: sp_mhc:*
- 7: sp_organelle:*
- 8: sp_phage:*
- 9: sp_plant:*
- 10: sp_rabbit:*
- 11: sp_rhodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: spUnclassified:*
- 15: sp_virus:*
- 16: sp_bacteria:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	53	15.4	238 2 099114	099114 escherichia
2	36	10.5	238 2 099123	099123 enterobacte
3	33	9.6	148 2 093Q01	093Q01 erwinia per
4	33	9.6	246 2 09L618	09L618 shigella fl
5	29	8.4	244 2 047880	047880 escherichia
6	29	8.4	244 2 099115	099115 escherichia
7	28	8.1	148 2 093QR2	093QR2 erwinia psi
8	28	8.1	148 2 093Q01	093Q01 erwinia psi
9	28	8.1	148 2 093Q00	093Q00 pectobacter
10	28	8.1	148 2 093Q00	093Q00 pectobacter
11	28	8.1	149 2 093Q04	093Q04 erwinia psi
12	28	8.1	149 2 093Q03	093Q03 erwinia psi
13	26	7.6	149 2 093Q02	093Q02 erwinia rho
14	22	6.4	147 2 093Q06	093Q06 brenneria r
15	22	6.4	149 2 093Q05	093Q05 erwinia mal
16	22	6.4	149 2 093Q04	093Q04 erwinia mal

17	18	6.4	22 19 6.4	0916J0 escherichia
22	22	6.4	21 20 6.1	08zg77 yersinia pe
23	21	6.1	21 21 6.1	093Qn8 erwinia chr
24	20	5.8	147 21 6.1	093Qp6 erwinia mal
25	20	5.8	147 21 6.1	093Qm4 erwinia tra
26	19	5.5	147 21 6.1	093Qm0 erwinia tra
27	19	5.5	147 21 6.1	093Qq7 brenneria r
28	19	5.5	149 21 6.1	093Qm1 salmonella
29	19	5.5	149 21 6.1	093Qm3 salmonella
30	19	5.5	149 21 6.1	093Qm2 salmonella
31	19	5.5	149 21 6.1	093Qm3 salmonella
32	19	5.5	149 21 6.1	093Qm2 salmonella
33	19	5.5	149 21 6.1	093Qm3 salmonella
34	19	5.5	149 21 6.1	093Qm2 salmonella
35	19	5.5	149 21 6.1	093Qm3 salmonella
36	19	5.5	149 21 6.1	093Qm2 salmonella
37	19	5.5	149 21 6.1	093Qm3 salmonella
38	19	5.5	149 21 6.1	093Qm2 salmonella
39	19	5.5	149 21 6.1	093Qm3 salmonella
40	19	5.5	149 21 6.1	093Qm2 salmonella
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42	19	5.5	149 21 6.1	093Qm2 salmonella
43	19	5.5	149 21 6.1	093Qm3 salmonella
44	19	5.5	149 21 6.1	093Qm2 salmonella
45	19	5.5	149 21 6.1	093Qm3 salmonella
46	19	5.5	149 21 6.1	093Qm2 salmonella
47	19	5.5	149 21 6.1	093Qm3 salmonella
48	19	5.5	149 21 6.1	093Qm2 salmonella
49	19	5.5	149 21 6.1	093Qm3 salmonella
50	19	5.5	149 21 6.1	093Qm2 salmonella
51	19	5.5	149 21 6.1	093Qm3 salmonella
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62	18	5.2	145 21 6.1	093Qm2 salmonella
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65	18	5.2	145 21 6.1	093Qm3 salmonella
66	18	5.2	145 21 6.1	093Qm2 salmonella
67	18	5.2	145 21 6.1	093Qm3 salmonella
68	18	5.2	145 21 6.1	093Qm2 salmonella
69	17	5.2	145 21 6.1	093Qm3 salmonella
70	17	4.9	147 21 6.1	093Qm69 erwinia car
71	16	4.7	147 21 6.1	093Qm79 brenneria r
72	15	4.4	145 21 6.1	093Qm0 brenneria n
73	15	4.4	145 21 6.1	093Qm99 brenneria l
74	15	4.4	145 21 6.1	093Qm8 brenneria n
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77	15	4.4	145 21 6.1	093Qm6 brenneria n
78	15	4.4	145 21 6.1	093Qm5 brenneria r
79	14	4.1	145 21 6.1	093Qp3 erwinia car
80	14	4.1	145 21 6.1	093Qm99 brenneria r
81	14	4.1	145 21 6.1	093Qm99 brenneria r
82	14	4.1	145 21 6.1	093Qm99 brenneria r
83	14	4.1	145 21 6.1	093Qm99 brenneria r
84	14	4.1	145 21 6.1	093Qm99 brenneria r
85	14	4.1	145 21 6.1	093Qm99 brenneria r
86	14	4.1	145 21 6.1	093Qm99 brenneria r
87	14	4.1	145 21 6.1	093Qm99 brenneria r
88	14	4.1	145 21 6.1	093Qm99 brenneria r
89	14	4.1	145 21 6.1	093Qm99 brenneria r

90	149	2	Q93Q56	erwinia amy	024350	silene lati
91	149	2	Q93Q54	erwinia amy	024350	escherichia
92	149	2	Q93Q53	erwinia amy	024350	oryza sativ
93	149	2	Q93Q52	erwinia amy	024350	Q57111 veillonella
94	149	2	Q93Q51	erwinia amy	024350	Q94A23 arabiopsis
95	149	2	Q93Q50	erwinia amy	024350	Q92T19 arabiopsis
96	147	2	Q93QNS	erwinia amy	024350	Q54030 propionigen
97	147	2	Q9AQ73	erwinia amy	024350	Q8rzw6 oryza sativ
98	149	2	Q93Q59	erwinia amy	024350	Q915a0 helicobacter
99	150	2	Q93Q59	pectobacter	024350	Q15192 caenorhabdi
100	147	2	Q93QH6	erwinia s	024350	Q9vrx77 drosophila
101	147	2	Q93QN4	erwinia s	024350	Q9ib35 katsuwonus
102	147	2	Q93QN3	erwinia s	024350	Q9zreg arabiopsis
103	147	2	Q93QN2	erwinia s	024350	Q9cbw9 mycobacteri
104	147	2	Q93QN1	erwinia s	024350	Q90w5 decapterus
105	10	2.9	106	2	Q93Q59	Q54279 sacharopol
106	10	2.9	236	5	Q9VW1	P09995 ceratitis c
107	10	2.9	339	2	Q93QH6	Q62008 ceratitis c
108	10	2.9	341	2	Q8RJ58	Q90895 gallus galli
109	10	2.9	344	2	Q8RMM2	Q91399 homo sapien
110	10	2.9	344	2	Q8RMH0	Q9zreg drosophila
111	10	2.9	344	2	Q9R659	Q9ay46 oryza sativ
112	10	2.9	344	2	Q9VW1	Q9ab4 cauliobacter
113	10	2.9	344	2	Q8RML8	Q9im2 streptomyce
114	10	2.9	346	2	Q8RJD0	Q9aats5 mycobacteri
115	10	2.9	346	2	Q9S5J9	Q9x00 ralstonia s
116	10	2.9	378	2	Q9RQ28	Q9vt6 streptomyce
117	9	2.6	146	2	Q93Q02	Q9ay1 streptomyce
118	9	2.6	146	2	Q93QQ1	Q93995 haemophilus
119	9	2.6	146	2	Q93Q01	Q90895 haemophilus
120	9	2.6	146	2	Q93Q09	Q91399 haemophilus
121	9	2.6	146	2	Q93Q09	Q91399 haemophilus
122	9	2.6	146	2	Q93Q09	Q91399 haemophilus
123	9	2.6	148	2	Q93Q09	Q91399 haemophilus
124	9	2.6	187	16	P74534	Q91399 haemophilus
125	9	2.6	191	13	Q9IB10	Q91399 haemophilus
126	9	2.6	192	13	Q9IB27	Q91399 haemophilus
127	9	2.6	193	13	Q9IB33	Q91399 haemophilus
128	9	2.6	193	13	Q90311	Q91399 haemophilus
129	9	2.6	193	13	Q90312	Q91399 haemophilus
130	9	2.6	194	13	Q90852	Q91399 haemophilus
131	9	2.6	194	13	Q90N44	Q91399 haemophilus
132	9	2.6	197	13	Q90466	Q91399 haemophilus
133	9	2.6	198	13	Q9TB39	Q91399 haemophilus
134	9	2.6	198	13	Q9IB36	Q91399 haemophilus
135	9	2.6	198	13	Q9W41	Q91399 haemophilus
136	9	2.6	203	13	Q12966	Q91399 haemophilus
137	9	2.6	215	10	Q43719	Q91399 haemophilus
138	9	2.6	249	2	Q9L575	Q91399 haemophilus
139	9	2.6	310	5	Q9W495	Q91399 haemophilus
140	9	2.6	326	2	Q9X450	Q91399 haemophilus
141	9	2.6	330	2	Q44299	Q91399 haemophilus
142	9	2.6	344	2	Q9LA97	Q91399 haemophilus
143	9	2.6	537	2	Q46977	Q91399 haemophilus
144	9	2.6	537	16	Q980A5	Q91399 haemophilus
145	9	2.6	581	5	Q20517	Q91399 haemophilus
146	9	2.6	403	2	P96774	Q91399 haemophilus
147	9	2.6	594	4	Q14772	Q91399 haemophilus
148	9	2.6	424	10	Q9FM65	Q91399 haemophilus
149	9	2.6	443	9	Q76153	Q91399 haemophilus
150	9	2.6	537	2	Q9RF11	Q91399 haemophilus
151	9	2.6	537	16	Q9VYT7	Q91399 haemophilus
152	9	2.6	1013	5	Q980A5	Q91399 haemophilus
153	9	2.6	1061	16	Q8X85	Q91399 haemophilus
154	9	2.6	1453	4	Q9Y671	Q91399 haemophilus
155	9	2.6	1606	11	Q92A2	Q91399 haemophilus
156	9	2.6	1608	4	Q96RK0	Q91399 haemophilus
157	9	2.6	1785	5	Q25685	Q91399 haemophilus
158	9	2.6	2163	9	Q9NF8	Q91399 haemophilus
159	9	2.6	2163	8	Q9VMZ2	Q91399 haemophilus
160	8	2.3	15	2	Q9RS64	Q91399 haemophilus
161	8	2.3	90	5	Q9VV28	Q91399 haemophilus
162	8	2.3	90	5	Q99L93	Q91399 haemophilus
163	8	2.3	164	8	Q86U0	Q91399 haemophilus
164	8	2.3	165	8	Q85017	Q91399 haemophilus
165	8	2.3	166	8	Q57111	Q91399 haemophilus
166	8	2.3	167	8	Q9A23	Q91399 haemophilus
167	8	2.3	168	8	Q92T19	Q91399 haemophilus
168	8	2.3	169	8	Q54030	Q91399 haemophilus
169	8	2.3	170	8	Q8RzW6	Q91399 haemophilus
170	8	2.3	171	8	Q9F6X6	Q91399 haemophilus
171	8	2.3	172	8	Q95192	Q91399 haemophilus
172	8	2.3	173	8	Q69087	Q91399 haemophilus
173	8	2.3	174	8	Q9EB35	Q91399 haemophilus
174	8	2.3	175	8	Q96B33	Q91399 haemophilus
175	8	2.3	176	8	Q90845	Q91399 haemophilus
176	8	2.3	177	8	Q54279	Q91399 haemophilus
177	8	2.3	178	8	Q9NFX6	Q91399 haemophilus
178	8	2.3	179	8	Q9VX77	Q91399 haemophilus
179	8	2.3	180	8	Q90895	Q91399 haemophilus
180	8	2.3	181	8	Q9399	Q91399 haemophilus
181	8	2.3	182	8	Q9RE9	Q91399 haemophilus
182	8	2.3	183	8	Q9CBW9	Q91399 haemophilus
183	8	2.3	184	8	Q9ABR4	Q91399 haemophilus
184	8	2.3	185	8	Q93N22	Q91399 haemophilus
185	8	2.3	190	8	Q93N22	Q91399 haemophilus
190	8	2.3	191	8	Q9ARAT5	Q91399 haemophilus
191	8	2.3	192	8	Q9IL137	Q91399 haemophilus
192	8	2.3	193	8	Q9RSN5	Q91399 haemophilus
193	8	2.3	194	8	Q9P2A6	Q91399 haemophilus
194	8	2.3	195	8	Q95X06	Q91399 haemophilus
195	8	2.3	196	8	Q9VZ7A	Q91399 haemophilus
196	8	2.3	197	8	Q9VX5	Q91399 haemophilus
197	8	2.3	198	8	Q91137	Q91399 haemophilus
198	8	2.3	199	8	Q9RSN5	Q91399 haemophilus
199	8	2.3	200	8	Q9P2A6	Q91399 haemophilus
200	8	2.3	201	8	Q95X06	Q91399 haemophilus
201	8	2.3	202	8	Q9VZ7A	Q91399 haemophilus
202	8	2.3	203	8	Q9S181	Q91399 haemophilus
203	8	2.3	204	8	Q9EWH8	Q91399 haemophilus
204	8	2.3	205	8	Q9B2Q2	Q91399 haemophilus
205	8	2.3	206	8	Q9S1F2	Q91399 haemophilus
206	8	2.3	207	8	Q9URC7	Q91399 haemophilus
207	8	2.3	208	8	Q9YI7	Q91399 haemophilus
208	8	2.3	209	8	Q9SXU6	Q91399 haemophilus
209	8	2.3	210	8	Q9XH1	Q91399 haemophilus
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211	8	2.3	212	8	Q93H0	Q91399 haemophilus
212	8	2.3	213	8	Q93953	Q91399 haemophilus
213	8	2.3	214	8	Q9SF90	Q91399 haemophilus
214	8	2.3	220	8	Q98B66	Q91399 haemophilus
220	8	2.3	221	8	Q96RXT7	Q91399 haemophilus
221	8	2.3	222	8	Q94GU0	Q91399 haemophilus
222	8	2.3	223	8	Q9H1X7	Q91399 haemophilus
223	8	2.3	224	8	Q92SX6	Q91399 haemophilus
224	8	2.3	225	8	Q925X6	Q91399 haemophilus
225	8	2.3	226	8	Q9325	Q91399 haemophilus
226	8	2.3	227	8	Q9326	Q91399 haemophilus
227	8	2.3	228	8	Q9327	Q91399 haemophilus
228	8	2.3	229	8	Q9328	Q91399 haemophilus
229	8	2.3	230	8	Q9329	Q91399 haemophilus
230	8	2.3	231	8	Q9330	Q91399 haemophilus
231	8	2.3	232	8	Q9331	Q91399 haemophilus
232	8	2.3	233	8	Q9332	Q91399 haemophilus
233	8	2.3	234	8	Q9333	Q91399 haemophilus
234	8	2.3	235	8	Q9334	Q91399 haemophilus
235	8	2.3	236	8	Q9335	Q91399 haemophilus
236	8	2.3	237	8	Q9336	Q91399 haemophilus
237	8	2.3	238	8	Q9337	Q91399 haemophilus
238	8	2.3	239	8	Q9338	Q91399 haemophilus
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240	8	2.3	241	8	Q9340	Q91399 haemophilus
241	8	2.3	242	8	Q9341	Q91399 haemophilus
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245	8	2.3	246	8	Q9345	Q91399 haemophilus
246	8	2.3	247	8	Q9346	Q91399 haemophilus
247	8	2.3	248	8	Q9347	Q91399 haemophilus
248	8	2.3	249	8	Q9348	Q91399 haemophilus
249	8	2.3	250	8	Q9349	Q91399 haemophilus
250	8	2.3	251	8	Q9350	Q91399 haemophilus
251	8	2.3	252	8	Q9351	Q91399 haemophilus
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254	8	2.3	255	8	Q9354	Q91399 haemophilus
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256	8	2.3	257	8	Q9356	Q91399 haemophilus
257	8	2.3	258	8	Q9357	Q91399 haemophilus
258	8	2.3	259	8	Q9358	Q91399 haemophilus
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260	8	2.3	261	8	Q9360	Q91399 haemophilus
261	8	2.3	262	8	Q9361	Q91399 haemophilus
262	8	2.3	263	8	Q9362	Q91399 haemophilus
263	8	2.3	264	8	Q9363	Q91399 haemophilus
264	8	2.3	265	8	Q9364	Q91399 haemophilus
265	8	2.3	266	8	Q9365	Q91399 haemophil

236	8	359	10	Q8Rxx9	zea mays (m	309	8	4	Q9P2x1	homo sapien		
237	8	360	2	Q86224	Q9f6w1	310	9	2.3	1046	oryza sativ		
238	8	361	12	Q9INR9	Q9yrm9	lymantria d	311	8	2.3	1046	Q9NRM7	
239	8	367	10	Q9LWE1	Q9jwv1	homo sapien	312	8	2.3	1088	Q9NRM7	
240	8	368	3	Q9PB837	Q9pw37	caenorhabdi	313	8	2.3	1097	Q9D2T9	
241	8	370	10	Q9SSW0	Q9sw0	oryza sativ	314	8	2.3	1098	Q9WTN8	
242	8	378	10	Q9SF49	Q9sf49	arabidopsis	315	8	2.3	1151	057580	
243	8	379	8	Q93991	Q93991	daucus caro	315	8	2.3	1154	Q9z1R2	
244	8	381	4	Q96075	Q9q15	homo sapien	316	8	2.3	1360	Q9P4Z2	
245	8	392	5	Q9V105	Q9v105	drosophila	317	8	2.3	1461	Q9T9F6	
246	8	394	2	Q9LAY6	Q9lay6	streptomyce	318	8	2.3	1474	Q9T4M0	
247	8	395	2	Q9LA21	Q9laz1	streptococc	319	8	2.3	1500	Q9V1LQ8	
248	8	395	2	Q9LAY2	Q9lay2	streptococc	320	8	2.3	1503	Q9t418	
249	8	399	16	Q9AP7	Q9xap7	escherichia	321	8	2.3	1509	Q9Sp10	
250	8	2.3	406	2	Q9LA20	Q9la20	streptococc	322	8	2.3	1513	Q97970
251	8	2.3	408	2	Q9LAY0	Q9lay0	streptococc	323	8	2.3	1553	Q95TRO
252	8	2.3	417	16	Q9PC63	Q9pc63	streptomyce	324	8	2.3	1584	Q93791
253	8	2.3	426	2	Q9LAY5	Q9lays	streptococc	325	8	2.3	1676	Q9TG36
254	8	2.3	437	16	Q9LAY4	Q9lay4	streptococc	326	8	2.3	1678	Q924C5
255	8	2.3	438	16	Q9A2W5	Q9a2w5	caulobacter	327	8	2.3	1698	Q9V5JB
256	8	2.3	439	10	Q9FWF7	Q9fwf7	oryza sativ	328	8	2.3	1785	Q8S789
257	8	2.3	440	2	Q9LAY1	Q9lay1	streptococc	329	8	2.3	1785	Q9VRA6
258	8	2.3	449	5	Q94M45	Q9m4c5	avena fatua	330	8	2.3	2110	Q96296
259	8	2.3	449	5	Q20198	Q20198	caenorhabdi	331	8	2.3	2197	Q96296
260	8	2.3	461	3	Q9X053	Q8x053	neurospora	332	8	2.3	2634	Q9JP78
261	8	2.3	468	6	Q9B2B3	Q9be23	maceca fasc	333	8	2.3	2689	Q8XSA40
262	8	2.3	468	10	Q9S5P0	Q9s5p0	oryza sativ	334	7	2.3	10917	Q93NW6
263	8	2.3	492	11	Q95392	Q95392	mus musculu	335	7	2.0	102	Q8W701
264	8	2.3	493	3	Q9UDY1	Q9udy1	orzya sativ	336	7	2.0	102	Q9F212
265	8	2.3	494	5	Q9M4C5	Q9m4c5	avena fatua	337	7	2.0	70	Q9S0T1
266	8	2.3	508	2	Q9B8A6	Q9fb74	deinococcus	338	7	2.0	83	Q9V8W6
267	8	2.3	533	4	Q9B5W9	Q9fb86	treponema p	339	7	2.0	94	Q9W618
268	8	2.3	542	12	Q91CH9	Q9hb59	homo sapien	340	7	2.0	102	Q9PXP5
269	8	2.3	552	10	Q96343	Q96343	macropodid	341	7	2.0	102	Q9PXP4
270	8	2.3	554	16	Q9X205	Q9x205	brassica na	342	7	2.0	108	Q9Y913
271	8	2.3	562	5	Q9TS2	Q9x205	pneumocysti	343	7	2.0	113	Q94503
272	8	2.3	569	10	Q9W204	Q9fb74	deinococcus	344	7	2.0	113	Q97222
273	8	2.3	581	5	Q9L1F6	Q9w82	oryza sativ	345	7	2.0	118	Q9X220
274	8	2.3	582	16	Q9AAQ8	Q9aqg8	drosophila	346	7	2.0	120	Q92BA0
275	8	2.3	584	16	Q9AAZ3	Q9aa23	caulobacter	347	7	2.0	121	Q9BDG2
276	8	2.3	590	16	Q9S2Q5	Q9s2q5	caulobacter	348	7	2.0	127	Q95RA0
277	8	2.3	596	16	Q9RSC6	Q9s9q5	streptomyce	349	7	2.0	129	Q90615
278	8	2.3	600	16	Q9HXJ8	Q9rc6	deinococcus	350	7	2.0	132	Q9SE04
279	8	2.3	605	16	Q9W204	Q9rhj8	pseudomonas	350	7	2.0	137	Q92T17
280	8	2.3	612	2	Q92E14	Q9fb86	streptomyce	351	7	2.0	139	Q8ZR5
281	8	2.3	643	10	Q23831	Q92e14	streptomyce	352	7	2.0	143	Q9H4U5
282	8	2.3	643	10	Q9SXH0	Q9s9q5	streptomyce	353	7	2.0	144	Q8U303
283	8	2.3	654	16	Q9RSC6	Q9s9q5	streptomyce	354	7	2.0	145	Q90615
284	8	2.3	667	2	Q9KK28	Q9rc6	deinococcus	355	7	2.0	147	Q9AA7
285	8	2.3	667	11	Q9R1D9	Q9hb18	streptomyce	356	7	2.0	155	Q97907
286	8	2.3	676	16	Q9XR9	Q9hb18	streptomyce	356	7	2.0	155	Q9BNK4
287	8	2.3	689	5	Q9GRF0	Q9rb18	streptomyce	357	7	2.0	156	Q9XEU0
288	8	2.3	693	16	Q9SXH0	Q9rc6	streptomyce	358	7	2.0	160	Q8TCG9
289	8	2.3	719	5	Q9NDT9	Q9s9q5	streptomyce	359	7	2.0	163	Q90W43
290	8	2.3	737	11	Q9WYF3	Q9rc6	treponema p	360	7	2.0	166	Q95268
291	8	2.3	739	2	Q9RQ74	Q9kb18	streptomyce	361	7	2.0	166	Q9AA7
292	8	2.3	744	16	Q9C2N3	Q9kb18	streptomyce	362	7	2.0	171	Q9C684
293	8	2.3	747	5	Q9XU12	Q9kb18	streptomyce	363	7	2.0	171	Q91b38
294	8	2.3	748	12	Q965820	Q9kb18	bovine herp	364	7	2.0	178	Q9D7T0
295	8	2.3	753	5	Q93107	Q9kb18	acanthamoeb	365	7	2.0	178	Q9SD3
296	8	2.3	784	16	Q9RK15	Q9kb18	thiobacillus	366	7	2.0	179	Q9SHY3
297	8	2.3	796	5	Q9VZB8	Q9kb18	drosophila	367	7	2.0	180	Q9SW3
298	8	2.3	806	11	Q9WVF4	Q9kb18	mus musculu	368	7	2.0	181	Q90W33
299	8	2.3	820	2	Q9RQ71	Q9kb18	streptomyce	369	7	2.0	182	Q9FB14
300	8	2.3	836	7	Q9SNA3	Q9kb18	streptomyce	370	7	2.0	187	Q9RCM7
301	8	2.3	860	5	Q9NDT9	Q9kb18	mus musculu	371	7	2.0	194	Q915B5
302	8	2.3	875	2	Q9RK15	Q9kb18	schizosacch	372	7	2.0	194	Q9W99
303	8	2.3	941	5	Q9FTX9	Q9kb18	streptomyce	373	7	2.0	194	Q904F1
304	8	2.3	963	3	Q43024	Q9kb18	schizosacch	374	7	2.0	194	Q9XAB0
305	8	2.3	1004	3	Q9HE23	Q9kb18	schizosacch	375	7	2.0	194	Q98477
306	8	2.3	1004	10	Q9LJ74	Q9kb18	schizosacch	376	7	2.0	204	Q9598
307	8	2.3	1015	5	Q9Y650	Q9kb18	schizosacch	377	7	2.0	204	Q9S2Q1
308	8	2.3	1023	4	Q92502	Q9kb18	schizosacch	378	7	2.0	206	Q9LVAS

382	2	Q9L593	streptococc	Q8trui methanosarc
383	7	209	10	Q9FPR2 vibrio chol
384	2.0	210	16	Q92981 salmonella
385	7	211	12	Q99GP7 culic nigeri
386	7	211	12	Q91909 culic nigeri
387	7	212	10	Q9M2D8 arabidopsis
388	7	212	12	Q41980 murid herpe
389	7	212	16	Q92KL1 rhizobium m
390	7	213	10	Q43600 oryza sativ
391	7	215	4	QUNGO hom sapien
392	7	222	2	Q9L584 streptococc
393	7	222	10	Q9S740 arabidopsis
394	7	223	5	Q9VY16 drosophila
395	7	223	5	Q17275 brugia paha
396	7	228	10	Q8S0R0 oryza sativ
397	7	231	5	Q9YKE4 drosophila
398	7	233	2	Q9L568 streptococc
399	7	236	2	Q9L569 streptococc
400	7	236	12	Q85028 pseudorabie
401	7	236	16	Q92BG4 listeria in
402	7	238	16	Q99Q6 streptomyce
403	7	239	10	Q94EG7 arabidopsis
404	7	242	2	Q9L562 streptococc
405	7	242	10	Q8RVE1 oryza sativ
406	7	243	2	Q9L567 streptococc
407	7	243	2	Q9L564 streptococc
408	7	244	2	Q9L565 streptococc
409	7	246	2	Q9L5B4 streptococc
410	7	246	2	Q9L578 streptococc
411	7	246	10	Q9LYW8 arabidopsis
412	7	247	2	Q9L566 streptococc
413	7	247	2	Q9L585 streptococc
414	7	249	2	Q9L570 streptococc
415	7	249	5	Q8TA41 heterocoda
416	7	249	10	Q9FKJ8 arabidopsis
417	7	249	10	Q94J05 oryza sativ
418	7	249	16	Q98M22 rhizobium l
419	7	251	16	Q98BC9 rhizobium l
420	7	252	10	Q9S2U5 arabidopsis
421	7	254	2	Q9L563 streptococc
422	7	255	2	Q9L5B6 streptococc
423	7	255	2	Q9L581 streptococc
424	7	255	4	Q9H3S2 homo sapien
425	7	255	10	Q9LGK5 oryza sativ
426	7	256	2	Q9L590 streptococc
427	7	257	2	Q9L594 streptococc
428	7	257	4	Q96JE6 homo sapien
429	7	258	16	Q9BR67 agrobacteri
430	7	258	16	Q9KA82 streptomyce
431	7	259	16	Q92SX7 rhizobium m
432	7	261	16	Q9JT72 neisseria m
433	7	262	16	Q9RTQ7 streptococc
434	7	265	16	Q8YUV1 anabana sp
435	7	265	16	Q8UD55 agrobacteri
436	7	275	2	Q8RKD3 erwinia chr
437	7	275	12	Q8V705 tulip band-
438	7	278	16	Q83418 pseudorabie
439	7	278	16	Q9RI59 zea mays (m
440	7	279	10	Q9CAS2 arabidopsis
441	7	282	16	Q8WMR7 clostridium
442	7	283	16	Q8XXN3 ralstonia s
443	7	286	2	Q9r640 mycobacteri
444	7	289	10	Q41824 zea mays (m
445	7	290	16	Q9QAO streptomyce
446	7	294	10	Q8W008 sorghum bic
447	7	296	5	Q9V729 drosophila
448	7	296	16	Q8T129 pseudomonas
449	7	297	10	Q41122 phaseolus v
450	7	305	16	Q8XUP6 ralstonia s
451	7	307	16	Q8UD56 agrobacteri
452	7	310	16	Q8Y2T9 ralstonia s
453	7	314	10	Q8S750 oryza sativ
454	7	317	4	Q96FB6 homo sapien
382	2.0	318	17	Q8TRU1
383	2.0	320	10	Q8SB33 oryza sativ
384	2.0	321	16	Q31154 vibrio chol
385	2.0	323	11	Q9EQ24 rattus norv
386	2.0	323	11	Q9eq2 ratus norv
387	2.0	325	2	Q9X4R7 pseudomonas
388	2.0	325	2	Q9X4R8 pseudomonas
389	2.0	327	10	Q9FWN19 oryza sativ
390	2.0	328	3	Q9UR34
391	2.0	329	11	Q9JK13
392	2.0	331	4	Q16509 homo sapien
393	2.0	331	5	Q9V728 drosophila
394	2.0	333	4	Q9NY94 homo sapien
395	2.0	335	5	Q8S2S4 drosophila
396	2.0	338	10	Q9SM99 arabidopsis
397	2.0	339	11	Q8RJ01
398	2.0	345	4	Q96IH2 homo sapien
399	2.0	347	16	Q9RR54 deinococcus
400	2.0	348	16	Q9RT15 deinococcus
401	2.0	349	11	Q9ERN9 mus musculu
402	2.0	350	10	Q9FM99 chlamydomydom
403	2.0	351	2	Q93TD8 pseudomonas
404	2.0	351	2	Q9TSZ5 drosophila
405	2.0	354	5	Q9VCN5 drosophila
406	2.0	354	10	Q9AT12 cibicory yel
407	2.0	354	16	Q84e3 salmonella
408	2.0	355	10	Q9LEZ5 streptomyces
409	2.0	356	16	Q8AY7 brucella me
410	2.0	356	17	Q8TgZ2 campylobact
411	2.0	357	16	Q9RW41 deinococcus
412	2.0	362	10	Q9AT58 cymbopogon
413	2.0	362	12	Q04325 cibicory yel
414	2.0	365	16	Q9ruh9 deinococcus
415	2.0	366	10	Q94339 arabidopsis
416	2.0	371	12	Q8V973 lily mottie
417	2.0	374	2	Q9FOF7 campylobact
418	2.0	375	16	Q9TM21 deinococcus
419	2.0	377	10	Q9FTN9 oryza sativ
420	2.0	380	2	Q9SA405 proteus mir
421	2.0	384	11	Q94D01 oryza sativ
422	2.0	384	11	Q9DAD1 mus musculu
423	2.0	388	5	Q9VMV9 drosophila
424	2.0	388	16	Q8B027 streptomyce
425	2.0	390	5	Q9VA28 drosophila
426	2.0	391	17	Q9Hz2 thermoplasm
427	2.0	392	17	Q9LAZ3 streptococc
428	2.0	393	11	Q9Jf4 mus musculu
429	2.0	398	2	Q9R1M1 streptomyce
430	2.0	399	5	Q9VHA1 drosophila
431	2.0	400	16	Q9ADJ6 streptomyces
432	2.0	401	2	Q9LaZ2 streptococc
433	2.0	404	10	Q9F5G5 arabiopsis
434	2.0	404	12	Q9IF26 cydia pomon
435	2.0	405	16	Q92MK3 rhizobium m
436	2.0	413	2	Q95077 streptomyce
437	2.0	416	2	Q9481 psychrobact
438	2.0	416	2	Q9pnP3 homo sapien
439	2.0	425	4	Q9HPW5 halobacteri
440	2.0	426	16	Q9uhh4 agarobacteri
441	2.0	428	16	Q9rip5 streptococc
442	2.0	430	16	Q8yr44 anabaena sp
443	2.0	431	10	Q8VZ63 arabidopsis
444	2.0	434	16	Q8RWB6 arabidopsis
445	2.0	435	10	Q9Suwl arabidopsis
446	2.0	436	4	Q9z2q2 homo sapien
447	2.0	437	10	Q9FDM2 oryza sativ
448	2.0	442	10	Q9LMR6 oryza sativ
449	2.0	444	10	Q96FB6 homo sapien

528	7	449	12	Q86537	tulip	break	Q965846	barley	yell
529	7	450	12	Q8QN85	Q8bn85	ectocarpus	Q9XK0	caenorhabdi	
530	7	453	7	Q86557	Q86557	moraxella	Q28883	archaeobacter	
531	7	455	5	Q61747	Q61747	caenorhabdi	Q9CKD9	pasturella	
532	7	457	16	Q92hc0	streptococc		Q9d2m6	mus	musculi
533	7	460	12	O12559	O12659	apple	Q9lTX1	arabidopsis	
534	7	469	4	Q99492	Q99492	homo	Q9fJ13	caenorhabdi	
535	7	470	2	Q9K3D7	Q9K3D7	moritella	Q9fJ13	arabidopsis	
536	7	475	5	Q9NG12	Q9Ng12	drosophila	Q9fJ13	arabidopsis	
537	7	475	5	Q9NG11	Q9Ng11	drosophila	Q9fJ13	arabidopsis	
538	7	475	5	Q9NG10	Q9Ng10	drosophila	Q9fJ13	arabidopsis	
539	7	475	16	Q8E746	Q8E746	drosophila	Q9fJ13	arabidopsis	
540	7	475	5	Q9N652	Q9N652	drosophila	Q9fJ13	arabidopsis	
541	7	475	5	Q9N656	Q9N656	drosophila	Q9fJ13	arabidopsis	
542	7	477	2	Q9W2X5	Q9w2x5	drosophila	Q9fJ13	arabidopsis	
543	7	479	2	Q9IA2X	Q9ia2x	streptococc	Q9pp16	campylobacte	
544	7	480	2	Q9LAX3	Q9laX3	streptococc	Q9pp16	campylobacte	
545	7	481	2	Q9LAX5	Q9laX5	streptococc	Q8r5f8	mus	musculi
546	7	486	16	Q8E746	Q8E746	streptococc	Q8tC11	homo	sapien
547	7	487	16	Q8XRH4	Q8xrh4	streptomyce	Q8vw85	homo	sapien
548	7	489	10	Q9SS90	Q9ss90	raistonia	Q19243	caenorhabdi	
549	7	494	10	Q9A814	Q9a814	arabidopsis	Q92496	mus	musculi
550	7	500	2	Q9LBT2	Q9lbT2	oriza	Q69743	mycobacteri	
551	7	508	16	Q9P72X3	Q9p72x3	sativ	Q9bzg1	homo	sapien
552	7	512	5	Q9WN14	Q9wn14	streptomyce	Q9fp683	neurospora	
553	7	513	3	Q9C1X4	Q9c1x4	drosophila	Q91092	streptomyce	
554	7	515	2	Q9LB70	Q9lb70	schizosacch	Q9pp2n8	homo	sapien
555	7	516	2	Q9kBT3	Q9kbT3	treponema	Q98q10	mycoplasma	
556	7	519	2	Q9RK20	Q9rk20	pseudot�able	Q8t1v7	methanobarc	
557	7	524	12	Q83417	Q83417	streptococc	Q92z01	arabidopsis	
558	7	524	16	Q9YR10	Q9yr10	streptomyce	Q9B683	neurospora	
559	7	526	12	Q85027	Q85027	deinococcus	Q9B683	neurospora	
560	7	526	12	Q85356	Q85356	pseudoradical	Q8uyt2	lilly	rottelle
561	7	528	2	Q9LB70	Q9lb70	treponema	Q8uzu2	Pyrococcus	
562	7	529	10	Q9FWD7	Q9fwD7	pseudot�able	Q8xy88	raistonia	s
563	7	538	16	Q8RI12	Q8ri12	streptococc	Q940956	pneumocysti	
564	7	540	12	Q69371	Q69371	fusobacteri	Q940956	caenorhabdi	
565	7	541	16	Q9RDM9	Q9rdm9	cercopithec	Q8yz24	raistonia	s
566	7	547	10	Q94GC1	Q94gc1	deinococcus	Q9v470	streptomyce	
567	7	551	16	Q9HUD4	Q9hud4	orzyza	Q9w328	raistonia	s
568	7	556	5	Q9RC6	Q9rc6	sativ	Q9y651	homo	sapien
569	7	556	16	Q53678	Q53678	mycobacteri	Q9y651	anabaena	sp
570	7	557	5	Q23933	Q23933	drosophila	Q9by75	rhizobium	1
571	7	566	11	Q9ERQ3	Q9erq3	mus	Q9by75	leishmania	
572	7	568	16	Q9RWU8	Q9rwu8	deinococcus	Q9by75	homo	sapien
573	7	570	6	Q28616	Q28616	oryctolagus	Q9by75	neurospora	
574	7	570	5	Q2PH1	Q2ph1	Q9apf5	Q9by75	equus	cabal
575	7	574	3	Q36027	Q36027	schizosacch	Q9by75	caenorhabdi	
576	7	574	5	Q17411	Q17411	aegyp	Q9by75	schizosacch	
577	7	574	16	Q9RTJ3	Q9rtj3	deinococcus	Q9by75	agrobacteri	
578	7	576	5	Q9VX72	Q9vx72	drosophila	Q9by75	anophelis	9
579	7	580	4	Q96ID0	Q96id0	homo	Q9by75	crofta	
580	7	584	16	Q9FCJ3	Q9fcJ3	sativ	Q9by75	neurospora	
581	7	586	10	Q40643	Q40643	oryza	Q9by75	equus	cabal
582	7	586	16	Q9L0T7	Q9l0t7	streptomyce	Q9by75	caenorhabdi	
583	7	587	10	Q23241	Q23241	arabidopsis	Q9by75	caenorhabdi	
584	7	587	16	Q9HUC8	Q9huc8	pseudomonas	Q9by75	caenorhabdi	
585	7	588	10	Q94BY3	Q94by3	caulobacter	Q9by75	caenorhabdi	
586	7	589	4	Q75148	Q75148	homo	Q9by75	caenorhabdi	
587	7	590	5	Q8Y088	Q8y088	sativ	Q9by75	caenorhabdi	
588	7	594	2	Q59099	Q59099	encephalito	Q9by75	caenorhabdi	
589	7	594	5	Q9VEP4	Q9vep4	alcaligenes	Q9by75	caenorhabdi	
590	7	595	4	Q9NXH0	Q9nxh0	Q9by75	caenorhabdi	trichosurus	
591	7	596	4	Q96BB7	Q96bb7	homo	Q9by75	leishmania	
592	7	596	11	Q9CVF3	Q9cvf3	homo	Q9by75	xenopus	lae
593	7	600	16	Q8Y088	Q8y088	mus	Q9by75	crofta	
594	7	606	4	Q9NPDU	Q9npu0	homo	Q9by75	anophelis	9
595	7	622	12	Q8V972	Q8v972	lilly	Q9by75	crofta	
596	7	626	3	Q9HFV3	Q9hfV3	ashbya	Q9by75	neurospora	
597	7	629	2	Q9KD56	Q9kd56	goss	Q9by75	trichosurus	
598	7	629	6	Q29426	Q29426	moritella	Q9by75	rattus	ratt
599	7	636	16	Q8UF8	Q8uf8	oryctolagus	Q9by75	danielio	dangi
600	7	640	16	Q06293	Q06293	agrobacteri	Q9by75	fugu	ruber

674	13	Q98SU4	danio	albol	Q91W0	mus	musculu			
675	7	977	13	Q98SU1	danio	nigro	Q8749	bacillus	ps	
676	7	978	6	Q9XS93	canis	famil	Q8344	capiscum	an	
677	7	978	11	Q63116	rattus	nory	Q9db3	bacillus	ha	
678	7	979	6	QBW23	canis	famil	Q83015	streptomyce		
679	7	995	11	Q35615	mus	musculu	Q9805	bacillus	ha	
680	7	1006	3	Q9C2A4	neurospora		Q9195	chonopodium		
681	7	1021	2	Q9KL56	actinoplane		Q9db9	oryza	sativ	
682	7	2.0	1039	5	Q9VWGB	drosophila		Q16428	caenorhabdi	
683	7	2.0	1053	4	Q96KJ4	homo	sepien	Q98kao	rhizobium	1
684	7	2.0	1087	5	Q96156	plasmoidium		Q9v5t4	drosophila	
685	7	2.0	1095	5	Q9U4G4	Q9u94	drosophila	Q96h0	drosophila	
686	7	2.0	1111	16	Q86522	streptomyce		Q82337	arabidopsis	
687	7	2.0	1132	16	Q9RRC7	deinococcus		Q9pad1	xylophilus	
688	7	2.0	1149	5	Q23315	caenorhabdi		Q8xxv9	ralstonia	s
689	7	2.0	1158	4	Q14113	homo	sapien	Q9yjb8	hepatitis	c
690	7	2.0	1172	5	Q9GZ10	caenorhabdi		Q56576	hepatitis	c
691	7	2.0	1264	5	P91767	P9167 manduca	sex	Q9ypq5	hepatitis	c
692	7	2.0	1272	16	Q9FBFR4	Q9ibr4	streptomyce	Q9ypq4	hepatitis	c
693	7	2.0	1274	4	Q9UM53	Q9um53	homo	Q9p1v5	campylobact	
694	7	2.0	1312	4	Q9NR59	Q9n59	homo	Q9pgg8	xylella	fas
695	7	2.0	1313	4	Q9C0C9	Q9cc9	homo	Q97c5	thermoplasm	
696	7	2.0	1343	4	Q9H7N4	Q9hn4	homo	Q62468	caenorhabdi	
697	7	2.0	1406	4	Q9Y216	Q9y16	homo	Q9u316	caenorhabdi	
698	7	2.0	1464	5	Q24132	Q24132 drosophila		Q9nbz2	trypanosoma	
699	7	2.0	1464	5	Q23995	Q23995 drosophila		Q8xxj9	ralstonia	s
700	7	2.0	1464	5	Q9VC47	Q9vc47 drosophila		Q9vml8	pseudomonas	
701	7	2.0	1663	4	Q9UQ01	Q9u01 homo	sapien	Q932n3	staphylococ	
702	7	2.0	1693	5	Q9W3P3	Q9wp3 drosophila		Q8yfv8	brucella	me
703	7	2.0	1711	5	Q95YX3	Q95yx3 leishmania		Q93b65	streptococ	
704	7	2.0	1714	10	Q941mt9	Q941mt9 oryza	sativ	Q93b22	arabidopsis	
705	7	2.0	1766	5	Q25668	Q25668 plasmodium		Q8vkh3	mycobacteri	
706	7	2.0	1777	10	Q941P9	Q94hp oryza	sativ	Q93b28	salmonella	
707	7	2.0	1819	10	Q8S2A4	Q8s2a4 oryza	sativ	Q933x5	salmonella	
708	7	2.0	1883	4	Q96SC5	Q9sc5 homo	sapien	Q9rsr2	deinococcus	
709	7	2.0	1905	4	Q96SC6	Q9sc6 homo	sapien	Q9jvng	nesseria	m
710	7	2.0	1929	5	Q9P3J0	Q9p3j0 neurospora		Q93aw8	salmonella	
711	7	2.0	1929	5	Q95WFO	Q90wf0 gallus	gall	Q9v6l1	hepatitis	c
712	7	2.0	2146	3	Q59897	Q59897 aspergillus		Q8vkh3	mycobacteri	
713	7	2.0	2146	3	Q60026	Q60026 aspergillus		Q93b28	salmonella	
714	7	2.0	2209	5	Q97124	Q97324 plasmodium		Q93b3	salmonella	
715	7	2.0	22184	5	Q22184	Q22184 caenorhabdi		Q93ay5	salmonella	
716	7	2.0	2408	5	Q965C6	Q965c6 homo	sapien	Q93ax8	salmonella	
717	7	2.0	2409	5	Q9P3J0	Q9p3j0 neurospora		Q9734	clostridium	
718	7	2.0	2446	3	Q59897	Q59897 leishmania		Q91899	bombyx	mori
719	7	2.0	3247	12	Q65553	Q65553 bovine	herp	Q9vq08	drosophila	
720	7	2.0	3261	4	Q9Y536	Q9y556 homo	sapien	Q93b22	salmonella	
721	7	2.0	3309	5	Q9GUP2	Q9gup2 caenorhabdi		Q93b12	salmonella	
722	7	2.0	35316	4	Q9V730	Q9v730 drosophila		Q9mbrr5	staphylococ	
723	7	2.0	3664	4	Q9V730	Q96t58 homo	sapien	Q8xit4	clostridium	
724	7	2.0	3192	2	Q91W4	Q91w4 streptomyce		Q97134	clostridium	
725	6	1.7	3247	12	Q65553	Q65553 bovine	herp	Q9vq08	diatom	
726	6	1.7	3261	4	Q9Y536	Q9y556 homo	sapien	Q93b28	salmonella	
727	6	1.7	27	5	Q7527	Q76527 holothuria		Q93b12	salmonella	
728	6	1.7	35	16	Q9QV88	Q99vb8 hepatitis	c	Q93b12	salmonella	
729	6	1.7	40	4	Q43072	Q913X8 mycoplasma		Q93b12	staphylococ	
730	6	1.7	50	2	Q9REL6	Q9rlp6 mycobacteri		Q93b12	staphylococ	
731	6	1.7	25	5	Q8t607	Q8t607 asterias	ru	Q93b12	staphylococ	
732	6	1.7	45	13	Q2DFK1	Q2dfk1 gillichthys		Q93b12	staphylococ	
733	6	1.7	48	16	Q9E67	Q9ue67 agrobacteri		Q93b12	vibrioph	chol
734	6	1.7	50	2	P81518	P81518 bacillus	th	Q8sdb8	bacterioph	
735	6	1.7	51	8	Q9XKE9	Q9xke9 grus	japon	Q92r9	arabidopsis	
736	6	1.7	53	16	Q8XCV5	Q8xcv5 salmonella	s	Q93b12	oryza	sativ
737	6	1.7	55	2	Q91B25	Q93b25 salmonella		Q93b12	salmonella	
738	6	1.7	58	16	Q9BDL6	Q9bd6 rhizobium	1	Q93b12	drosophila	
739	6	1.7	59	2	Q9F2J8	Q9f2j8 streptomyce		Q93b12	arabidopsis	
740	6	1.7	61	10	Q859S5	Q8s95 oryza	sativ	Q93b12	oryza	sativ
741	6	1.7	61	12	Q8V1C3	Q8v1c3 hepatitis	c	Q93b12	senecio	vul
742	6	1.7	61	12	Q8V1C2	Q8v1c2 hepatitis	c	Q93b12	parina	nuda
743	6	1.7	61	12	Q8V1CO	Q8v1c0 hepatitis	c	Q93b12	salmonella	
744	6	1.7	62	4	Q9P1AS	Q9p1a5 homo	sapien	Q93ay0	salmonella	
745	6	1.7	65	4	Q9Y2U1	Q9y2u1 homo	sapien	Q93ay0	oryza	sativ
746	6	1.7	66	2	Q93AX5	Q93ax5 salmonella		Q93ay0	oryza	sativ

820	6	1.7	97	10	Q9FTN1	09ftn1 oryza sativ	Q9mj14 carabus gen	6	1.7	8	Q9MJJ4
821	6	1.7	98	2	Q93B71	Q93B71 salmonella	Q9mj13 carabus coa	894	895	6	Q9MJJ3
822	6	1.7	98	5	Q9VRG2	Q9vr92 drosophilila	Q9mj12 carabus abb	895	896	6	Q9MJJ2
823	6	1.7	98	5	Q8ZW7	Q8zw7 pyrobaculum	Q9mj11 carabus can	896	897	6	Q9MJJ1
824	6	1.7	98	17	Q8B434	Q8B434 leptospira	Q9mj10 carabus arv	897	898	6	Q9MJJ0
825	6	1.7	99	2	Q68436	Q68436 leptospira	Q9mj19	899	900	6	Q9MJJ9
826	6	1.7	99	2	Q93B57	Q93B57 salmonella	Q9xhd clostridium	900	900	6	Q8xhd0 salmonella
827	6	1.7	100	2	Q93AV9	Q93av9 salmonella	Q93b23 salmonella	900	901	6	Q93b23
828	6	1.7	100	2	Q93B57	Q93B57 arabidopsis	Q9d2cl mus musculus	900	902	6	Q9d2cl
829	6	1.7	100	10	Q9SMH7	Q9smh7 salmonella	Q9neq5 caenorhabdi	900	903	6	Q9neq5
830	6	1.7	101	2	Q93B4	Q93b44 salmonella	Q9mj01 carabous	900	904	6	Q9mj01
831	6	1.7	101	12	Q9IAN2	Q9ian2 hepatitis b	Q9mj10 carabus can	900	905	6	Q9mj10
832	6	1.7	102	2	Q93AW5	Q9aw5 salmonella	Q9mj19	900	906	6	Q9mj19
833	6	1.7	103	2	Q93B52	Q93b52 salmonella	Q91u87 hepatitis b	900	906	6	Q91u87
834	6	1.7	103	2	Q93AV3	Q93av3 salmonella	Q91u86 hepatitis b	900	907	6	Q91u86
835	6	1.7	103	2	Q93B56	Q93b56 microscilla	Q91u85 hepatitis b	900	908	6	Q91u85
836	6	1.7	104	2	Q93B29	Q93b29 salmonella	Q91u86 hepatitis b	900	909	6	Q91u86
837	6	1.7	104	10	Q9LFV3	Q9lpv3 arabidopsis	Q91u85 hepatitis b	900	909	6	Q91u85
838	6	1.7	104	16	Q8VR36	Q8vr36 anabena sp	Q91u85 hepatitis b	900	910	6	Q91u85
839	6	1.7	104	17	Q9HL12	Q9hl12 thermoplasm	Q91u85 hepatitis b	900	911	6	Q91u85
840	6	1.7	105	2	Q9AN17	Q9an17 bradyrhizob	Q91u85 hepatitis b	900	912	6	Q91u85
841	6	1.7	105	2	Q93B67	Q93b67 salmonella	Q91u85 hepatitis b	900	913	6	Q91u85
842	6	1.7	105	2	Q93B53	Q93b53 salmonella	Q91u85 hepatitis b	900	914	6	Q91u85
843	6	1.7	105	2	Q93B26	Q93b26 salmonella	Q91u85 hepatitis b	900	915	6	Q91u85
844	6	1.7	105	2	Q93AX9	Q93ax9 salmonella	Q91u85 hepatitis b	900	916	6	Q91u85
845	6	1.7	105	5	Q9NA56	Q9na56 caenorhabdi	Q91u85 hepatitis b	900	917	6	Q91u85
846	6	1.7	105	8	Q9GT44	Q9gt44 convoluta c	Q91u85 hepatitis b	900	918	6	Q91u85
847	6	1.7	105	10	Q93B67	Q93b67 salmonella	Q91u85 hepatitis b	900	919	6	Q91u85
848	6	1.7	105	10	Q93B73	Q93b73 salmonella	Q91u85 hepatitis b	900	920	6	Q91u85
849	6	1.7	107	2	Q93B38	Q93b38 salmonella	Q91u85 hepatitis b	900	921	6	Q91u85
850	6	1.7	107	2	Q93Q3	Q93q3 salmonella	Q91u85 hepatitis b	900	922	6	Q91u85
851	6	1.7	107	16	Q9ADC4	Q9adc4 streptomyce	Q91u85 hepatitis b	900	923	6	Q91u85
852	6	1.7	108	2	Q9JB78	Q9jb78 lactococcus	Q91u85 hepatitis b	900	924	6	Q91u85
853	6	1.7	108	6	Q93ST8	Q9xst8 canis famili	Q91u85 hepatitis b	900	925	6	Q91u85
854	6	1.7	108	10	Q9FVY4	Q9fv4 oryza sativ	Q91u85 hepatitis b	900	926	6	Q91u85
855	6	1.7	108	16	Q99S54	Q99s54 oryza sativ	Q91u85 hepatitis b	900	927	6	Q91u85
856	6	1.7	108	16	Q9CE28	Q9ce28 staphylococ	Q91u85 hepatitis b	900	928	6	Q91u85
857	6	1.7	109	2	Q9JB61	Q9jb61 salmonella	Q91u85 hepatitis b	900	929	6	Q91u85
858	6	1.7	109	5	Q9YV10	Q9yv10 drosophila	Q91u85 hepatitis b	900	930	6	Q91u85
859	6	1.7	109	10	Q9W5F8	Q9wf8 oryza sativ	Q91u85 hepatitis b	900	931	6	Q91u85
860	6	1.7	109	10	Q94CY1	Q94cy1 oryza sativ	Q91u85 hepatitis b	900	932	6	Q91u85
861	6	1.7	109	12	Q91300	Q91300 hepatitis c	Q91u85 hepatitis b	900	933	6	Q91u85
862	6	1.7	109	12	Q81452	Q81452 hepatitis c	Q91u85 hepatitis b	900	934	6	Q91u85
863	6	1.7	109	12	Q81459	Q81459 hepatitis c	Q91u85 hepatitis b	900	935	6	Q91u85
864	6	1.7	109	12	Q81301	Q81301 hepatitis c	Q91u85 hepatitis b	900	936	6	Q91u85
865	6	1.7	109	12	Q81482	Q81482 hepatitis c	Q91u85 hepatitis b	900	937	6	Q91u85
866	6	1.7	109	12	Q81298	Q81298 hepatitis c	Q91u85 hepatitis b	900	938	6	Q91u85
867	6	1.7	109	12	Q81543	Q81543 hepatitis c	Q91u85 hepatitis b	900	939	6	Q91u85
868	6	1.7	109	12	Q81545	Q81545 hepatitis c	Q91u85 hepatitis b	900	940	6	Q91u85
869	6	1.7	109	12	Q81802	Q81802 hepatitis c	Q91u85 hepatitis b	900	941	6	Q91u85
870	6	1.7	109	12	Q81804	Q81804 hepatitis c	Q91u85 hepatitis b	900	942	6	Q91u85
871	6	1.7	110	12	Q93B55	Q93b55 archaeoglob	Q91u85 hepatitis b	900	943	6	Q91u85
872	6	1.7	110	2	Q93B14	Q93b14 salmonella	Q91u85 hepatitis b	900	944	6	Q91u85
873	6	1.7	110	12	Q93C1	Q93c1 salmonella	Q91u85 hepatitis b	900	945	6	Q91u85
874	6	1.7	110	12	Q9DWK2	Q9dwk2 hepatitis c	Q91u85 hepatitis b	900	946	6	Q91u85
875	6	1.7	111	2	Q93B77	Q93b77 salmonella	Q91u85 hepatitis b	900	947	6	Q91u85
876	6	1.7	111	2	Q93B03	Q93b03 salmonella	Q91u85 hepatitis b	900	948	6	Q91u85
877	6	1.7	111	8	Q9MJJ7	Q9mj7 campalita m	Q91u85 hepatitis b	900	949	6	Q91u85
878	6	1.7	111	12	Q67928	Q67928 hepatitis hb	Q91u85 hepatitis b	900	950	6	Q91u85
879	6	1.7	111	12	Q93B72	Q93b72 hepatitis b	Q91u85 hepatitis b	900	951	6	Q91u85
880	6	1.7	111	12	Q67931	Q67931 hepatitis b	Q91u85 hepatitis b	900	952	6	Q91u85
881	6	1.7	111	2	Q93B42	Q93b42 hepatitis b	Q91u85 hepatitis b	900	953	6	Q91u85
882	6	1.7	112	2	Q93B00	Q93b00 hepatitis b	Q91u85 hepatitis b	900	954	6	Q91u85
883	6	1.7	113	10	Q92NZ2	Q92nz2 petunia hyb	Q91u85 hepatitis b	900	955	6	Q91u85
884	6	1.7	114	2	Q93B13	Q93b13 salmonella	Q91u85 hepatitis b	900	956	6	Q91u85
885	6	1.7	114	2	Q93A26	Q93a26 hepatitis c	Q91u85 hepatitis b	900	957	6	Q91u85
886	6	1.7	114	2	Q93A25	Q93a25 hepatitis c	Q91u85 hepatitis b	900	958	6	Q91u85
887	6	1.7	114	2	Q93B09	Q93b09 hepatitis b	Q91u85 hepatitis b	900	959	6	Q91u85
888	6	1.7	114	15	Q39132	Q39132 human immun	Q91u85 hepatitis b	900	960	6	Q91u85
889	6	1.7	115	2	Q92B27	Q92bz2 salmonella	Q91u85 hepatitis b	900	961	6	Q91u85
890	6	1.7	115	2	Q93AY1	Q93ay1 salmonella	Q91u85 hepatitis b	900	962	6	Q91u85
891	6	1.7	115	8	Q9TK97	Q9tk97 kochia scop	Q91u85 hepatitis b	900	963	6	Q91u85
892	6	1.7	115	8	Q9MJJ7	Q9mj7 carabus nit	Q91u85 hepatitis b	900	964	6	Q91u85

966 6 1.7 128 10 Q9LJZ4 Pinus taeda
967 6 1.7 128 10 Q943d8 Oriza sativa
968 6 1.7 129 2 Q93B00
969 6 1.7 129 2 Q93B18
970 6 1.7 129 2 Q93B22
971 6 1.7 129 2 Q93A4
972 6 1.7 129 2 Q93AW6
973 6 1.7 129 16 Q8Ym4
974 6 1.7 130 2 Q93B16
975 6 1.7 130 2 Q93B68
976 6 1.7 130 10 Q40603
977 6 1.7 130 16 Q05839
978 6 1.7 131 2 Q93B04
979 6 1.7 131 2 Q93AW7
980 6 1.7 131 5 Q9VvZ7
981 6 1.7 131 10 Q9SJY7
982 6 1.7 131 12 Q40906
983 6 1.7 132 2 Q9EYt9
984 6 1.7 132 2 Q93B75
985 6 1.7 132 2 Q93B56
986 6 1.7 132 2 Q93A28
987 6 1.7 132 8 Q93Ax3
988 6 1.7 133 12 Q9Yt2
989 6 1.7 133 12 Q80SP8
990 6 1.7 134 2 Q93B37
991 6 1.7 134 2 Q93AX3
992 6 1.7 135 2 Q93BA7
993 6 1.7 136 16 P22919
994 6 1.7 137 2 Q93B58
995 6 1.7 137 2 Q9AGt8
996 6 1.7 138 2 Q9F6Y0
997 6 1.7 138 2 Q93B54
998 6 1.7 138 2 Q93Ax2
999 6 1.7 138 16 Q92A17
1000 6 1.7 138 16 Q8YtQ9

ALIGNMENTS

RESULT 1
ID 099114 PRELIMINARY; PRT; 238 AA.
AC 099114; (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 15, Last annotation update)
DE Outer membrane protein A (Outer membrane protein II) (Fragment).
GN Escherichia vulneris.
OS Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
NCBI_TAXID=566;
RN SEQUENCE FROM N.A.; STRAIN=ATCC 29943;
RC MEDLINE=90065222; PubMed=1955870;
RA "Molecular and evolutionary relationships among enteric bacteria.";
RL J. Gen. Microbiol. 137:191-1921(1991).
CC -I- SUBCELLULAR LOCATION: OUTER MEMBRANE.
DR EMBL; HSSP; P02934; AAA24233.1;
DR InterPro; IPR01145; Bac_OmpA.
DR PRINTS; PR01389; OmpA_mem.
DR Pfam; PF00691; OmpA; 1.
DR PROSITE; PR01021; OMPADOMAIN.
DR PROSITE; PS01068; OMPA; 1.
DR NON_TER 1 1
SQ SEQUENCE 238 AA; 25553 MW; BCDF6AF25240502B CRC64;
Query Match Score 10.5%; Best Local Similarity 100.0%; Pred. No. 6e-28; Length 238;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 2
ID Q99123 PRELIMINARY; PRT; 238 AA.
AC 099123; (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE Outer membrane protein A (Outer membrane protein II) (Fragment).
GN OmpA.
OS Enterobacter aerogenes (Aerobacter aerogenes).
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Enterobacter; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OX NCBI_TAXID=548;
RN HSSP; P02934; 1QJP;
DR InterPro; IPR001145; Bac_OmpA.
DR PRINTS; PR01021; OMPADOMAIN.
DR Pfam; PF00691; OmpA; 1.
DR PRODOM; PD000930; Bac_OmpA; 1.
DR PROSITE; PS01068; OMPA; 1.
DR NON_TER 1 1
SQ SEQUENCE 238 AA; 25553 MW; BCDF6AF25240502B CRC64;
Query Match Score 36; Best Local Similarity 100.0%; Pred. No. 6e-28; Length 238;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 3
ID Q93QPI PRELIMINARY; PRT; 148 AA.
AC 093QPI; (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Major outer membrane protein (Fragment).
GN OmpA.
OS Erwinia persicina.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Erwinia.
OX NCBI_TAXID=55221;
RN [1];
RP SEQUENCE FROM N.A.;
RC STRAIN=33998;
RA Brown E.W., Davis R.M., Gouk C., van der Zwet T.;

"Allelic diversity of the major outer membrane protein (ompA) gene among necroticogenic phytopathogenic species: Molecular evolutionary aspects of relatedness."

Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.

NCBI_TaxID=566;

SEQUENCE FROM N.A.

STRAIN=ATCC 33821; AND ATCC 33822;

MEDLINE=92065252; PubMed=1955870;

RA Lawrence J.G.; Ochman H.; Hartl D.L.;

RT "Molecular and evolutionary relationships among enteric bacteria.";

J. Gen. Microbiol. 137:1911-1921(1991).

DR EMBL: M63350; AAA24241.1; -

DR HSSP: P02934; 1QJP

DR InterPro: IPR01145; Bac_OmpA.

DR InterPro: IPR00498; OmpA_tmem.

DR Pfam: PF00691; OmpA_1.

DR PRINTS: PRO1021; OMPADOMAIN.

DR PRODom: PD000930; Bac_OmpA_1.

DR PROSITE: PS01068; OMPA_1.

DR PTM: PT01389; OmpA_membrane; 1.

DR RSLT: RSLT001; OMPADOMAIN.

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RESULT 7
 Q93QR2 PRELIMINARY; PRT; 148 AA.
 ID Q93QR2; AC Q93QR2; NCBI_TAXID=69224;
 OC Erwinia; RN [1];
 SEQUENCE FROM N.A.
 STRAIN=EP8427;
 RA Brown E.W., Davis R.M., Gouk C., van der Zwart T.;
 RT "Allelic diversity of the major outer membrane protein (ompA) gene
 among necrogenic phytopathogenic species: Molecular evolutionary
 aspects of relatedness.";
 RT Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
 RL EMBL; AF220780; AAK68946 1.;
 DR InterPro; IPR01115; Bac_OmpA.
 DR InterPro; IPR00498; OmpA_tnem.
 DR Pfam; PF00691; OmpA; 1.
 DR Pfam; PF001389; OmpA_membrane; 1.
 DR ProDom; PD000030; Bac_OmpA; 1.
 FT NON_TER 1 148 AA; 16410 MW; 2BBD1FAC6530167F CRC64;
 SQ SEQUENCE 148 AA; 16410 MW;

Query Match Best Local Similarity 8.1%; Score 28; DB 2; Length 148;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 217 SDVLFNFNKATLKPEQQALDQLYTOLS 244
 Db 111 SDVLFNFNKATLKPEQQALDQLYTOLS 138

RESULT 8
 Q93QR1 PRELIMINARY; PRT; 148 AA.
 ID Q93QR1; AC Q93QR1; NCBI_TAXID=69224;
 OC Erwinia; RN [1];
 SEQUENCE FROM N.A.
 STRAIN=EP8406;
 RA Brown E.W., Davis R.M., Gouk C., van der Zwart T.;
 RT "Allelic diversity of the major outer membrane protein (ompA) gene
 among necrogenic phytopathogenic species: Molecular evolutionary
 aspects of relatedness.";
 RT Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
 RL EMBL; AF220781; AAK68947 1.;
 DR InterPro; IPR001145; Bac_OmpA.
 DR InterPro; IPR00098; OmpA; 1.
 DR Pfam; PF001389; OmpA_membrane; 1.
 DR ProDom; PD000030; Bac_OmpA; 1.
 FT NON_TER 1 148 AA; 16040 MW; 73DDA11D6DFAAB00 CRC64;

Query Match Best Local Similarity 100.0%; Score 28; DB 2; Length 148;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 217 SDVLFNFNKATLKPEQQALDQLYTOLS 244
 Db 111 SDVLFNFNKATLKPEQQALDQLYTOLS 138

RESULT 9
 Q93QR0 PRELIMINARY; PRT; 148 AA.
 ID Q93QR0; AC Q93QR0; NCBI_TAXID=69224;
 OC Erwinia; RN [1];
 SEQUENCE FROM N.A.
 STRAIN=EP358;
 RA Brown E.W., Davis R.M., Gouk C., van der Zwart T.;
 RT "Allelic diversity of the major outer membrane protein (ompA) gene
 among necrogenic phytopathogenic species: Molecular evolutionary
 aspects of relatedness.";
 RT Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
 RL EMBL; AF220782; AAK68948 1.;
 DR InterPro; IPR001145; Bac_OmpA.
 DR InterPro; IPR000498; OmpA_tnem.
 DR Pfam; PF00691; OmpA; 1.
 DR ProDom; PD0000930; Bac_OmpA; 1.
 FT NON_TER 1 148 AA; 16410 MW; 2BBD1FAC6530167F CRC64;

Query Match Best Local Similarity 100.0%; Score 28; DB 2; Length 148;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 217 SDVLFNFNKATLKPEQQALDQLYTOLS 244
 Db 111 SDVLFNFNKATLKPEQQALDQLYTOLS 138

RESULT 10
 Q93QP0 PRELIMINARY; PRT; 148 AA.
 ID Q93QP0; AC Q93QP0; NCBI_TAXID=55209;
 OC Pectobacterium cypripedii. RN [1];
 SEQUENCE FROM N.A.
 STRAIN=EP8427;
 RA Brown E.W., Davis R.M., Gouk C., van der Zwart T.;
 RT "Allelic diversity of the major outer membrane protein (ompA) gene
 among necrogenic phytopathogenic species: Molecular evolutionary
 aspects of relatedness.";
 RT Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
 RL EMBL; AF220802; AAK68968 1.;
 DR InterPro; IPR01145; Bac_OmpA.
 DR InterPro; IPR00098; OmpA; 1.
 DR Pfam; PF001389; OmpA_membrane; 1.
 DR ProDom; PD000030; Bac_OmpA; 1.
 FT NON_TER 1 148 AA; 16040 MW; 73DDA11D6DFAAB00 CRC64;

Query Match Best Local Similarity 100.0%; Score 28; DB 2; Length 148;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 217 SDVLFNFNKATLKPEQQALDQLYTOLS 244
 Db 111 SDVLFNFNKATLKPEQQALDQLYTOLS 138

aspects of relatedness.";

RT Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.

RL "Allelic diversity of the major outer membrane protein (ompA) gene among necrogenic phytopathogenic species: Molecular evolutionary aspects of relatedness.";

DR EMBL; AF220779; AAK68945; 1;

DR InterPro; IPR01145; Bac_OmpA;

DR InterPro; IPR00498; OmpA_tmem.

DR Pfam; PF00691; OmpA; 1.

DR Pfam; PF01389; OmpA_tmem.

DR PDDOM; PD0000330; Bac_OmpA; 1.

FT NON-TER 1

FT NON-TER 149 AA; 149 MW; 16346 MW; 4422BFA4550541D5 CRC64;

SQ SEQUENCE 112 DVLFENKATLKPBCQQALDQLYTLSN 245

Query Match Score 8.1%; DB 2; Length 148;

Best Local Similarity 100.0%; Pred. No. 5e-20;

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 112 DVLFENKATLKPBCQQALDQLYTLSN 139

RESULT 11

ID Q93QR4 PRELIMINARY; PRT; 149 AA.

AC Q93QR4;

DT 01-DEC-2001 (TREMBLel. 19, Created)

DT 01-DEC-2001 (TREMBLel. 19, Last sequence update)

DT 01-JUN-2002 (TREMBLel. 21, Last annotation update)

DE Major outer membrane protein (Fragment).

GN OMPA.

OS Erwinia psidii.

OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;

OC Erwinia.

OX NCBI_TAXID=69224;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=EP429;

RA Brown E.W., Davis R.M., Gouk C., van der Zwart T.;

RT "Allelic diversity of the major outer membrane protein (ompA) gene among necrogenic phytopathogenic species: Molecular evolutionary aspects of relatedness.";

RT Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.

RL EMBL; AF220778; AAK68944; 1;

DR InterPro; IPR01145; Bac_OmpA;

DR InterPro; IPR00498; OmpA_tmem.

DR Pfam; PF00691; OmpA; 1.

DR Pfam; PF01389; OmpA_tmem.

DR PRODOM; PRO000930; Bac_OmpA; 1.

FT NON-TER 149 AA; 149 MW; 16380 MW; 5472FFA455195DD5 CRC64;

SQ SEQUENCE 112 DVLFENKATLKPBCQQALDQLYTLSN 245

Query Match Score 8.1%; DB 2; Length 149;

Best Local Similarity 100.0%; Pred. No. 5.1e-20;

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 112 DVLFENKATLKPBCQQALDQLYTLSN 139

RESULT 12

ID Q93QR3 PRELIMINARY; PRT; 149 AA.

AC Q93QR3;

DT 01-DEC-2001 (TREMBLel. 19, Created)

DT 01-DEC-2001 (TREMBLel. 19, Last sequence update)

DT 01-JUN-2002 (TREMBLel. 21, Last annotation update)

DE Major outer membrane protein (Fragment).

GN OMPA.

OS Erwinia psidii.

CC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;

CC Erwinia.

OX NCBI_TAXID=69224;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=EP428;

RA Brown E.W., Davis R.M., Gouk C., van der Zwart T.;

RT "Allelic diversity of the major outer membrane protein (ompA) gene among necrogenic phytopathogenic species: Molecular evolutionary aspects of relatedness.";

RT Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.

RL EMBL; AF220800; AAK68946; 1;

DR InterPro; IPR01145; Bac_OmpA;

DR InterPro; IPR00498; OmpA_tmem.

DR Pfam; PF00691; OmpA; 1.

DR Pfam; PF01389; OmpA_tmem.

DR PRODOM; PD0000330; Bac_OmpA; 1.

FT NON-TER 149 AA; 149 MW; 16004 MW; 8E0064C39DFEAFF216 CRC64;

SQ SEQUENCE 149 AA; 149 MW; 16004 MW; 8E0064C39DFEAFF216 CRC64;

Query Match Score 7.6%; DB 2; Length 149;

Best Local Similarity 100.0%; Pred. No. 5.4e-18;

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 115 LFENKATLKPBCQQALDQLYTLSN 140

RESULT 13

ID Q93QR2 PRELIMINARY; PRT; 149 AA.

AC Q93QR2;

DT 01-DEC-2001 (TREMBLel. 19, Created)

DT 01-DEC-2001 (TREMBLel. 19, Last sequence update)

DT 01-JUN-2002 (TREMBLel. 21, Last annotation update)

DE Major outer membrane protein (Fragment).

GN OMPA.

OS Brenneria rubrifaciens.

CC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;

CC Brenneria.

OX NCBI_TAXID=69224;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=EP428;

RA Brown E.W., Davis R.M., Gouk C., van der Zwart T.;

RT "Allelic diversity of the major outer membrane protein (ompA) gene among necrogenic phytopathogenic species: Molecular evolutionary aspects of relatedness.";

RT Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.

RL EMBL; AF220801; AAK68947; Bac_OmpA;

DR InterPro; IPR01145; Bac_OmpA;

DR InterPro; IPR00498; OmpA_tmem.

DR Pfam; PF00691; OmpA; 1.

DR Pfam; PF01389; OmpA_tmem.

DR PRODOM; PD0000330; Bac_OmpA; 1.

FT NON-TER 149 AA; 149 MW; 16004 MW; 8E0064C39DFEAFF216 CRC64;

SQ SEQUENCE 149 AA; 149 MW; 16004 MW; 8E0064C39DFEAFF216 CRC64;

Query Match Score 7.6%; DB 2; Length 149;

Best Local Similarity 100.0%; Pred. No. 5.4e-18;

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 115 LFENKATLKPBCQQALDQLYTLSN 140

RESULT 14

ID Q93QR6 PRELIMINARY; PRT; 147 AA.

AC Q93QR6;

DT 01-DEC-2001 (TREMBLel. 19, Created)

DT 01-DEC-2001 (TREMBLel. 19, Last sequence update)

DT 01-JUN-2002 (TREMBLel. 21, Last annotation update)

DE Major outer membrane protein (Fragment).

GN OMPA.

OS Brenneria rubrifaciens.

CC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;

CC Brenneria.

OX NCBI_TAXID=69224;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=EP428;

RA Brown E.W., Davis R.M., Gouk C., van der Zwart T.;

RT "Allelic diversity of the major outer membrane protein (ompA) gene among necrogenic phytopathogenic species: Molecular evolutionary aspects of relatedness.";

RT Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.

RL EMBL; AF220802; AAK68948; Bac_OmpA;

DR InterPro; IPR01145; Bac_OmpA;

DR InterPro; IPR00498; OmpA_tmem.

DR Pfam; PF00691; OmpA; 1.

DR Pfam; PF01389; OmpA_tmem.

DR PRODOM; PD0000330; Bac_OmpA; 1.

FT NON-TER 149 AA; 149 MW; 16004 MW; 8E0064C39DFEAFF216 CRC64;

SQ SEQUENCE 149 AA; 149 MW; 16004 MW; 8E0064C39DFEAFF216 CRC64;

Query Match Score 7.6%; DB 2; Length 149;

Best Local Similarity 100.0%; Pred. No. 5.4e-18;

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 115 LFENKATLKPBCQQALDQLYTLSN 140

OX NCBI_TAXID=55213;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BR4790;
 RA Brown E.W., Davis R.M., Gouk C., van der Zwart T.;
 RT "Allelic diversity of the major outer membrane protein (ompA) gene
 among necrogenic phytopathogenic species: Molecular evolutionary
 aspects of relatedness.";
 RT Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
 RL EMBL; AF220786; AAK63952.1;
 DR InterPro; IPR001145; Bac_OmpA.
 DR InterPro; IPR000498; OmpA_tmem.
 DR Pfam; PF00691; OmpA; 1.
 DR Pfam; PF01389; OmpA_membrane; 1.
 FT NON-TER 1 1
 FT NON-TER 147 147
 SQ SEQUENCE 147 AA; 16020 MW; 92F131FC1442DC4 CRC64;
 Query Match 6.4%; Score 22; DB 2; Length 147;
 Best Local Similarity 100.0%; Pred. No. 6.2e-14;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 213 FTLKSDVLFNFNKATLKPEQQ 234
 Db 106 FTLKSDVLFNFNKATLKPEQQ 127

RESULT 15

Q93QPS
 ID Q93QPS PRELIMINARY; PRT; 149 AA.
 AC Q93QPS;
 DT 01-DEC-2001 (TREMBREL 19, Created)
 DT 01-JUN-2002 (TREMBREL 21, Last sequence update)
 DE Major outer membrane protein (Fragment).
 GN OMPA.
 OS Erwinia maliotivora.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Erwinia.
 OX NCBI_TAXID=6922;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=EM8645;
 RA Brown E.W., Davis R.M., Gouk C., van der Zwart T.;
 RT "Allelic diversity of the major outer membrane protein (ompA) gene
 among necrogenic phytopathogenic species: Molecular evolutionary
 aspects of relatedness.";
 RT Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
 RL EMBL; AF220797; AAK63963.1;
 DR InterPro; IPR001145; Bac_OmpA.
 DR InterPro; IPR000498; OmpA_tmem.
 DR Pfam; PF00691; OmpA; 1.
 DR Pfam; PF01389; OmpA_membrane; 1.
 DR ProDom; PD000930; Bac_OmpA; 1.
 FT NON-TER 1 1
 FT NON-TER 149 149
 SQ SEQUENCE 149 AA; 16100 MW; 3494978343ED9A6C CRC64;
 Query Match 6.4%; Score 22; DB 2; Length 149;
 Best Local Similarity 100.0%; Pred. No. 6.3e-14;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 223 FNKATLKPEQQALDQLYTLS 244
 Db 118 FNKATLKPEQQALDQLYTLS 139

Search completed: April 15, 2003, 08:56:27
 Job time : 71 secs